WEST

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Search Results - Record(s) 1 through 10 of 16 returned.

1. Document ID: US 20020040490 A1

L1: Entry 1 of 16 File: PGPB Apr 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020040490
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020040490 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US CL-CURRENT: 800/288; 435/4, 536/23.2, 536/23.6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

2. Document ID: US 20020040489 A1

L1: Entry 2 of 16 File: PGPB Apr 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020040489
PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020040489 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Fricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288; 435/4, 536/23.2, 536/23.6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWMC | Draw Desc | Image

3. Document ID: US 20020023280 A1

L1: Entry 3 of 16 File: PGPB Feb 21, 2002

PGPUB-DOCUMENT-NUMBER: 20020023280
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020023280 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: February 21, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE 47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Fricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288; 435/4, 536/23.2, 536/23.6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

4. Document ID: US 20010051335 A1

L1: Entry 4 of 16 File: PGPB Dec 13, 2001

PGPUB-DOCUMENT-NUMBER: 20010051335
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

PUBLICATION-DATE: December 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
LALGUDI, RAGHUNATH V.	CLAYTON	MO	US	
ITO, LAURA Y.	PLEASANTON	CA	US	
SHERMAN, BRADLEY K.	OAKLAND	CA	US	

US-CL-CURRENT: 435/6; 435/69.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

5. Document ID: US 6368848 B1

L1: Entry 5 of 16 File: USPT

US-PAT-NO: 6368848
DOCUMENT-IDENTIFIER: US 6368848 B1

TITLE: Compositions to identify plant proteins that function in G-protein coupled systems

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

6. Document ID: US 6333403 B1

L1: Entry 6 of 16 File: USPT

US-PAT-NO: 6333403
DOCUMENT-IDENTIFIER: US 6333403 B1

TITLE: Chromosome 17p-linked prostate cancer susceptibility gene and a paralog and orthologous genes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

7. Document ID: US 6294348 B1

L1: Entry 7 of 16 File: USPT

US-PAT-NO: 6294348
DOCUMENT-IDENTIFIER: US 6294348 B1

TITLE: TRAF inhibitors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

8. Document ID: US 6090784 A

L1: Entry 8 of 16 File: USPT

US-PAT-NO: 6090784
DOCUMENT-IDENTIFIER: US 6090784 A

TITLE: RNA polymerase II peptides and methods of use

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

9. Document ID: US 6060303 A

L1: Entry 9 of 16 File: USPT

US-PAT-NO: 6060303
DOCUMENT-IDENTIFIER: US 6060303 A

TITLE: TRAF inhibitors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

10. Document ID: US 6004553 A

L1: Entry 10 of 16 File: USPT

US-PAT-NO: 6004553
DOCUMENT-IDENTIFIER: US 6004553 A

TITLE: TRAF inhibitors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

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Term	Documents
ARABIDOPSIS.DWPI,EPAB,JPAB,USPT,PGPB.	2648
ARABIDOPSI.DWPI,EPAB,JPAB,USPT,PGPB.	3
KINASE.DWPI,EPAB,JPAB,USPT,PGPB.	29622
KINASES.DWPI,EPAB,JPAB,USPT,PGPB.	6986
SHAGGY.DWPI,EPAB,JPAB,USPT,PGPB.	475
SHAGGIES	0
SHAGGYS	0
ASK.DWPI,EPAB,JPAB,USPT,PGPB.	13293
ASKS.DWPI,EPAB,JPAB,USPT,PGPB.	10359
(ARABIDOPSIS AND (SHAGGY OR ASK) AND KINASE).USPT,PGPB,JPAB,EPAB,DWPI.	16
(ARABIDOPSIS AND KINASE AND (SHAGGY OR ASK)).USPT,PGPB,JPAB,EPAB,DWPI.	16

Display Format: - Change Format

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Search Results - Record(s) 11 through 16 of 16 returned.

11. Document ID: US 5989897 A

L1: Entry 11 of 16 File: USPT

US-PAT-NO: 5989897
DOCUMENT-IDENTIFIER: US 5989897 A

TITLE: Yeast silencing genes proteins and methods

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

12. Document ID: US 5985584 A

L1: Entry 12 of 16 File: USPT

US-PAT-NO: 5985584
DOCUMENT-IDENTIFIER: US 5985584 A

TITLE: Method to identify plant proteins that function in G protein coupled systems and compositions therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

13. Document ID: US 5789550 A

L1: Entry 13 of 16 File: USPT

US-PAT-NO: 5789550
DOCUMENT-IDENTIFIER: US 5789550 A

TITLE: TRAF inhibitors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

14. Document ID: US 5599670 A

L1: Entry 14 of 16 File: USPT

US-PAT-NO: 5599670
DOCUMENT-IDENTIFIER: US 5599670 A

TITLE: .beta.-glucuronidase and glucuronide permease gene system

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

15. Document ID: US 5432081 A

L1: Entry 15 of 16 File: USPT

US-PAT-NO: 5432081
DOCUMENT-IDENTIFIER: US 5432081 A

TITLE: Host cells transformed with the E. coli glucoronide permease gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

16. Document ID: US 5268463 A

L1: Entry 16 of 16 File: USPT

US-PAT-NO: 5268463
DOCUMENT-IDENTIFIER: US 5268463 A

TITLE: Plant promoter .alpha.-glucuronidase gene construct

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

Generate Collection | Print

Term	Documents
ARABIDOPSIS.DWPI,EPAB,JPAB,USPT,PGPB.	2648
ARABIDOPSI.DWPI,EPAB,JPAB,USPT,PGPB.	3
KINASE.DWPI,EPAB,JPAB,USPT,PGPB.	29622
KINASES.DWPI,EPAB,JPAB,USPT,PGPB.	6986
SHAGGY.DWPI,EPAB,JPAB,USPT,PGPB.	475
SHAGGIES	0
SHAGGYS	0
ASK.DWPI,EPAB,JPAB,USPT,PGPB.	13293
ASKS.DWPI,EPAB,JPAB,USPT,PGPB.	10359
(ARABIDOPSIS AND (SHAGGY OR ASK) AND KINASE).USPT,PGPB,JPAB,EPAB,DWPI.	16
(ARABIDOPSIS AND KINASE AND (SHAGGY OR ASK)).USPT,PGPB,JPAB,EPAB,DWPI.	16

Display Format: - Change Format

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? s arabidopsis and kinas?
          95824  ARABIDOPSIS
         903032  KINAS?
      S1     7347  ARABIDOPSIS AND KINAS?
? s s1 and shaggy
           7347  S1
            824  SHAGGY
      S2      90  S1 AND SHAGGY
? s s1 and ask
           7347  S1
         216778  ASK
      S3      55  S1 AND ASK
? s s1 and /zeta
>>>Character "/" in invalid position
? s s1 and ?zeta
>>>File 155 processing for ?ZETA stopped at ALOGRAFT
>>>File 5 processing for ?ZETA stopped at ACTIVASTING
>>>File 6 processing for ?ZETA stopped at AUTOCC
>>>File 10 processing for ?ZETA stopped at ANIAMA
>>>File 34 processing for ?ZETA stopped at ADIABATIC MECHANISM     j  >
>>>File 44 processing for ?ZETA stopped at BAHAMA I., FRESH CREEK
<------User Break------>
u
? s s1 and dzeta
           7347  S1
            214  DZETA
      S4       0  S1 AND DZETA
? s s1 and zeta
           7347  S1
          40199  ZETA
      S5      21  S1 AND ZETA
? rd s2
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...examined 50 records  (50)
...completed examining records
      S6      28  RD S2 (unique items)
? t s6/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

 6/3,AB/1      (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12907072   21678988   PMID: 11820813
    The   UCU1  Arabidopsis  gene  encodes  a  SHAGGY/GSK3-like
kinase required for cell expansion along the proximodistal axis.
  Perez-Perez Jose Manuel; Ponce Maria Rosa; Micol Jose Luis
  Division de Genetica and Instituto de Bioingenieria, Universidad Miguel
Hernandez, Campus de Elche, 03202 Elche, Alicante, Spain.
  Developmental biology (United States)  Feb 15 2002,  242  (2)  p161-73,
ISSN 0012-1606  Journal Code: 0372762
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Most  signal  transduction pathways central to development are not shared
by  plants  and  animals.  Such  is  the case of the Wingless/Wnt signaling
pathway,  whose components play key roles in metazoan pattern formation and
tumorigenesis, but are absent in plants, with the exception of SHAGGY
/GSK3,  a  cytoplasmic  protein  kinase  represented in the genome of
Arabidopsis  thaliana  by  a  family  of  10  AtSK  genes  for  which
```

mutational evidence is scarce. Here, we describe the characterization of mutant alleles of the **Arabidopsis** ULTRACURVATA1 (UCU1) gene, the two strongest of which dramatically reduce cell expansion along the proximodistal axis, dwarfing the mutant plants, whose cells expand properly across but not along most organs. Proximodistal expansion of adaxial (dorsal) and abaxial (ventral) leaf cells exhibits a differential dependence on UCU1 function, as suggested by the leaves of ucu1 mutants, which are rolled spirally downward in a circinate manner. We have positionally cloned the UCU1 gene, which encodes an AtSK protein involved in the cross-talk between auxin and brassinosteroid signaling pathways, as indicated by the responses of ucu1 mutants to plant hormones and the phenotypes of double mutants involving ucu1 alleles.

6/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12922630 21836537 PMID: 11847343
Regulation of brassinosteroid signaling by a GSK3/**SHAGGY**-like **kinase**.
Li Jianming; Nam Kyoung Hee
Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI 48109-1048, USA.
Science (United States) Feb 15 2002, 295 (5558) p1299-301, ISSN 1095-9203 Journal Code: 0404511
Contract/Grant No.: GM60519; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
GSK3/**SHAGGY** is a highly conserved serine/threonine **kinase** implicated in many signaling pathways in eukaryotes. Although many GSK3/**SHAGGY**-like **kinases** have been identified in plants, little is known about their functions in plant growth and development. Here we show that the **Arabidopsis** BRASSINOSTEROID-INSENSITIVE 2 (BIN2) gene encodes a GSK3/**SHAGGY**-like **kinase**. Gain-of-function mutations within its coding sequence or its overexpression inhibit brassinosteroid (BR) signaling, resulting in plants that resemble BR-deficient and BR-response mutants. In contrast, reduced BIN2 expression via cosuppression partially rescues a weak BR-signaling mutation. Thus, BIN2 acts as a negative regulator to control steroid signaling in plants.

6/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12544189 21425095 PMID: 11532176
Constitutive over-expression of AtGSK1 induces NaCl stress responses in the absence of NaCl stress and results in enhanced NaCl tolerance in **Arabidopsis**.
Piao H L; Lim J H; Kim S J; Cheong G W; Hwang I
Center for Plant Intracellular Trafficking, Pohang University of Science and Technology, Pohang, 790-784, Korea.
Plant journal : for cell and molecular biology (England) Aug 2001, 27 (4) p305-14, ISSN 0960-7412 Journal Code: 9207397
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
GSK3/**shaggy**-like protein **kinases** have been shown to play diverse roles in development and signal transduction pathways in various organisms. An **Arabidopsis** homologue of GSK3/**shaggy**-like **kinase**, AtGSK1, has been shown to be involved in NaCl stress responses. In order to further clarify the role of AtGSK1 in NaCl stress

responses in plants, we generated transgenic **Arabidopsis** plants that over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl stress when assayed either as whole plants or by measurement of root growth on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of NaCl stress showed phenotypic changes, such as accumulation of anthocyanin, that were similar to those observed in wild-type plants under NaCl stress. Transgenic plants accumulated 30-50% more Na+ than did wild-type plants when subjected to NaCl stress, and Ca2+ content was increased by 15-30% in the transgenic plants regardless of the NaCl stress level. Northern blotting revealed that AtGSK1 over-expression induced expression of the NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl stress. In addition, AtCBL1 and AtCP1 were super-induced in the NaCl-stressed transgenic plants. Taken together, these results suggest that AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress responses in **Arabidopsis**.

6/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10692632 20223136 PMID: 10758494
Arabidopsis thaliana **SHAGGY**-related protein **kinases** (AtSK11 and 12) function in perianth and gynoecium development.
Dornelas M C; Van Lammeren A A; Kreis M
Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP), UMR/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France.
Plant journal : for cell and molecular biology (ENGLAND) Mar 2000, 21 (5) p419-29, ISSN 0960-7412 Journal Code: 9207397
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis SHAGGY** -related protein **kinase** genes AtSK11 (ASKalpha) and AtSK12(ASKgamma). The AtSK genes are plant homologues of the Drosophila **shaggy** (SGG) gene and the mammalian Glycogen-Synthase **Kinase**-3 (GSK-3). The SGG protein **kinase** is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASKalpha) and AtSK12(ASKgamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASKalpha) and AtSK12(ASKgamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASKalpha) and AtSK12(ASKgamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

6/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10219761 99214484 PMID: 10198112
An **Arabidopsis** GSK3/**shaggy**-like gene that complements yeast salt stress-sensitive mutants is induced by NaCl and abscisic acid.
Piao H L; Pih K T; Lim J H; Kang S G; Jin J B; Kim S H; Hwang I
Department of Molecular Biology, Biotechnology Research Center, Gyeongsang National University, Chinju, 660-701, Korea.

Plant physiology (UNITED STATES) Apr 1999, 119 (4) p1527-34, ISSN 0032-0889 Journal Code: 0401224
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

GSK3/**shaggy**-like genes encode **kinases** that are involved in a variety of biological processes. By functional complementation of the yeast calcineurin mutant strain DHT22-1a with a NaCl stress-sensitive phenotype, we isolated the **Arabidopsis** cDNA AtGSK1, which encodes a GSK3/**shaggy**-like protein **kinase**. AtGSK1 rescued the yeast calcineurin mutant cells from the effects of high NaCl. Also, the AtGSK1 gene turned on the transcription of the NaCl stress-inducible PMR2A gene in the calcineurin mutant cells under NaCl stress. To further define the role of AtGSK1 in the yeast cells we introduced a deletion mutation at the MCK1 gene, a yeast homolog of GSK3, and examined the phenotype of the mutant. The mck1 mutant exhibited a NaCl stress-sensitive phenotype that was rescued by AtGSK1. Also, constitutive expression of MCK1 complemented the NaCl-sensitive phenotype of the calcineurin mutants. Therefore, these results suggest that Mck1p is involved in the NaCl stress signaling in yeast and that AtGSK1 may functionally replace Mck1p in the NaCl stress response in the calcineurin mutant. To investigate the biological function of AtGSK1 in **Arabidopsis** we examined the expression of AtGSK1. Northern-blot analysis revealed that the expression is differentially regulated in various tissues with a high level expression in flower tissues. In addition, the AtGSK1 expression was induced by NaCl and exogenously applied ABA but not by KCl. Taken together, these results suggest that AtGSK1 is involved in the osmotic stress response in **Arabidopsis**.

6/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10155524 99178801 PMID: 10080716

Characterization of three novel members of the **Arabidopsis** **SHAGGY**-related protein **kinase** (ASK) multigene family.

Dornelas M C; Wittich P; von Recklinghausen I; van Lammeren A; Kreis M

Institut de Biotechnologie des Plantes EP3/CNRS 569, Universite de Paris-Sud, Orsay, France.

Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47, ISSN 0167-4412 Journal Code: 9106343
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

In this paper we report the characterization of three novel members of the **Arabidopsis** **shaggy**-related protein **kinase** (ASK) multigene family, named ASKdzeta (ASKzeta), ASKetha (ASKeta) and ASKiota (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to **SHAGGY** (SGG) and glycogen synthase **kinase**-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein **kinases** demonstrated a clear distinction between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect

biochemical and/or biological properties of these **kinases** . The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

6/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10039177 99023747 PMID: 9804971
An evolutionary conserved group of plant GSK-3/**shaggy**-like protein **kinase** genes preferentially expressed in developing pollen.
Dantinsky G; Tavares R; Takvorian A; Schwebel-Dugue N; Twell D; Kreis M
Institut de Biotechnologie des Plantes, Laboratoire de Biologie du Developpement des Plantes, Batiment 630, Universite de Paris-Sud CNRS/ERS 569, F-91405 Orsay Cedex, France.
Biochimica et biophysica acta (NETHERLANDS) Nov 8 1998, 1442 (2-3) p261-73, ISSN 0006-3002 Journal Code: 0217513
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Genes and cDNAs encoding plant protein **kinases** highly homologous to the animal GSK-3/**shaggy** subfamily were isolated from **Arabidopsis** thaliana, Brassica napus, Petunia hybrida and Nicotiana tabacum using the P. hybrida PSK6 GSK-3/**shaggy** related cDNA as a probe. All the derived protein sequences contained the characteristic catalytic domain of GSK-3/**shaggy** protein **kinases**. Sequence comparisons within the catalytic domain with other plant GSK-3/**shaggy** like **kinases** clearly indicate that the novel sequences form an isolated group of genes termed the PSK6 group. All the proteins within this group possess an amino-terminal extension which contains short amino acid motifs highly conserved between species and possibly implicated in mitochondrial targeting. Northern hybridisation experiments and reverse transcriptase PCR analysis demonstrated that these novel cDNAs are predominantly expressed in developing pollen. The three genes isolated from P. hybrida and A. thaliana show the same genomic organisation into 12 introns and 13 exons. Although the size of the introns varies, their positions are conserved between genes and species. The comparison of these gene structures and the analysis of deduced protein sequences belonging to different plants hold important information to understand the function of individual members. They suggest that some of the characterised sequences represent most likely true orthologues whereas others must be paralogues. They also allow us to discuss the evolution of the plant GSK-3/**shaggy** like gene family with regard to plant speciation.

6/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09842008 98278841 PMID: 9611268
The **Arabidopsis** **SHAGGY**-related protein **kinase** (ASK) gene family: structure, organization and evolution.
Dornelas M C; Lejeune B; Dron M; Kreis M
Institut de Biotechnologie des Plantes, ERS/CNRS 569, Universite de Paris-Sud, Batiment 630, F-91405, Orsay, Cedex, France.
Gene (NETHERLANDS) Jun 8 1998, 212 (2) p249-57, ISSN 0378-1119 Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein **kinase** domain about 70% identical to **SHAGGY** protein **kinase** (SGG) and glycogen synthase **kinase** -3 (GSK-3), respectively, from Drosophila and mammals. In this study we have characterized the structure and evolution of the **Arabidopsis SHAGGY**-related protein **kinase** (ASK) gene family. At least ten ASK genes are present per haploid genome of **Arabidopsis** . The genomic sequences of five ASK genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the **Arabidopsis** gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted ASK genes were mapped and shown to be dispersed over the five **Arabidopsis** chromosomes. A tentative model for the organization and evolution of the **Arabidopsis** ASK genes is presented.

6/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08425409 95178552 PMID: 7873606
Isolation and expression during pollen development of a tobacco cDNA clone encoding a protein **kinase** homologous to **shaggy**/glycogen synthase **kinase**-3.
Einzenberger E; Eller N; Heberle-Bors E; Vicente O
Institute of Microbiology and Genetics, University of Vienna, Austria.
Biochimica et biophysica acta (NETHERLANDS) Feb 21 1995, 1260 (3) p315-9, ISSN 0006-3002 Journal Code: 0217513
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
We have isolated a tobacco (Nicotiana tabacum L.) cDNA clone encoding a putative serine/threonine protein **kinase** , which shows highest homology to previously described families of alfalfa and **Arabidopsis** protein **kinases** and to their homologues rat glycogen synthase **kinase**-3 and Drosophila **shaggy kinases** . Northern experiments showed that NtK-4 is expressed in all sporophytic tobacco tissues tested, as well as in gametophytic and embryogenic pollen.

6/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08422393 95170005 PMID: 7865793
Inflorescence-specific expression of AtK-1, a novel **Arabidopsis** thaliana homologue of **shaggy**/glycogen synthase **kinase**-3.
Jonak C; Heberle-Bors E; Hirt H
Institute of Microbiology and Genetics, University of Vienna, Vienna Biocenter, Austria.
Plant molecular biology (NETHERLANDS) Jan 1995, 27 (1) p217-21, ISSN 0167-4412 Journal Code: 9106343
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
We report here the isolation of the **Arabidopsis** thaliana gene AtK-1. The predicted protein sequence of AtK-1 shows 70% identity to the **Arabidopsis** ASK and alfalfa MsK **kinases** that are homologs of the Drosophila **shaggy** and rat GSK-3 serine/threonine protein **kinases** playing an important role in signal transduction processes in animals. Northern analysis of different organs revealed exclusive expression in inflorescences suggesting an involvement of the AtK-1

kinase in reproduction-specific processes.

6/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08026635 94150468 PMID: 7509023
Arabidopsis homologs of the **shaggy** and GSK-3 protein **kinases** : molecular cloning and functional expression in Escherichia coli.
Bianchi M W; Guivarc'h D; Thomas M; Woodgett J R; Kreis M
Centre de Recherches sur les Plantes URA 1128, Universite de Paris-Sud, Orsay, France.
Molecular & general genetics : MGG (GERMANY) Feb 1994, 242 (3) p337-45, ISSN 0026-8925 Journal Code: 0125036
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The conservation in evolution of fundamental signal transduction modules offers a means of isolating genes likely to be involved in plant development. We have amplified by PCR **Arabidopsis** cDNA and genomic sequences related to the product of the **shaggy**/zeste-white 3 (sgg) segment polarity gene of Drosophila. This regulatory protein is functionally homologous to glycogen synthase **kinase**-3 in mammals (GSK-3), which regulates, among others, the DNA-binding activity of the c-jun/AP1 transcription factor. Analysis of PCR products led to the identification of five genes; for two of which, corresponding full-length cDNAs, ASK-alpha and gamma (for **Arabidopsis shaggy**-related protein **kinase**), were characterized. The encoded proteins were 70% identical to GSK-3 and sgg over the protein **kinase** catalytic domain and, after production in Escherichia coli, autophosphorylated mainly on threonine and serine residues, but phosphotyrosine was also detected. ASK-alpha and ASK-gamma also phosphorylated phosphatase inhibitor-2 and myelin basic protein, on threonine and serine, respectively. The high conservation of the protein **kinases** of GSK-3 family, and their action at the transcriptional level, suggest that the ASK proteins have important functions in higher plants.

6/3,AB/12 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

13554801 BIOSIS NO.: 200200183622
Non-purified anti-peptide sera generate tissue specific artefacts in immunohistochemical staining of **Arabidopsis** thaliana.
AUTHOR: Tavares R; Vidal J; van Lammeren A; Kreis M(a)
AUTHOR ADDRESS: (a)Institut de Biotechnologie des Plantes (IBP), Universite de Paris-Sud, UMR CNRS 8618, Batiment 630, 91405, Orsay Cedex**France
E-Mail: kreis@ibp.u-psud.fr
JOURNAL: Plant Science (Shannon) 162 (2):p309-314 February, 2002
MEDIUM: print
ISSN: 0168-9452
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Polyclonal antibodies raised against short synthetic peptides require coupling of the peptide to a larger carrier molecule before immunisation. A significant fraction of the total antibody pool of the serum from the immunised animal corresponds to carrier-specific antibodies, which may generate tissue specific artefacts not detected with the pre-immune sera. Using four non-purified anti-peptide sera,

corresponding to specific amino-terminal domains of four different **Arabidopsis** thaliana **SHAGGY** like **kinases** (AtSKs), we demonstrated that the obtained immunohistochemical staining patterns are not related to the peptide specific antibodies. The purification of the anti-peptide antibodies allowed the elimination of the artefactual tissue specific labelling, and revealed a completely different protein localisation. Hence, removal of non-specific antibodies from the immune serum is essential when performing immunohistochemical studies.

2002

6/3,AB/13 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

09606211 BIOSIS NO.: 199598061129
Arabidopsis homologues of the **shaggy**/GSK-3 protein **kinase**

AUTHOR: Bianchi Michele W; Guivarc'h Dominique; Kreis Martin
AUTHOR ADDRESS: Biologie Developpement Plantes, Bat. 430, Univ. Paris-Sud, F-91405 Orsay Cedex**France
JOURNAL: Acta Botanica Gallica 140 (6):p708
CONFERENCE/MEETING: Meeting of the Botanical Society of France on the Molecular and Cellular Bases of Morphogenesis in Plants Paris, France December 5, 1992
RECORD TYPE: Citation
LANGUAGE: English

6/3,AB/14 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA
(c) format only 2002 The Dialog Corporation. All rts. reserv.

39711423 23240936 Holding Library: AGL
Constitutive over-expression of AtGSK1 induces NaCl stress responses in the absence of NaCl stress and results in enhanced NaCl tolerance in **Arabidopsis**
Piao, H.L. Lim, J.H.; Kim, S.J.; Cheong, G.W.; Hwang, I.
Oxford : Blackwell Sciences Ltd.
The Plant journal : for cell and molecular biology. Aug 2001. v. 27 (4) p. 305-314.
ISSN: 0960-7412
DNAL CALL NO: QK710.P68
Language: English
GSK3/**shaggy**-like protein **kinases** have been shown to play diverse roles in development and signal transduction pathways in various organisms. An **Arabidopsis** homolcgue of GSK3/**shaggy**-like **kinase**, AtGSK1, has been shown to be involved in NaCl stress responses. In order to further clarify the role of AtGSK1 in NaCl stress responses in plants, we generated transgenic **Arabidopsis** plants that over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl stress when assayed either as whole plants or by measurement of root growth on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of NaCl stress showed phenotypic changes, such as accumulation of anthocyanin, that were similar to those observed in wild-type plants under NaCl stress. Transgenic plants accumulated 30-50% more Na+ than did wild-type plants when subjected to NaCl stress, and Ca(2+) content was increased by 15-30% in the transgenic plants regardless of the NaCl stress level. Northern blotting revealed that AtGSK1 over-expression induced expression of the NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl stress. In addition, AtCBL1 and AtCP1 were super-induced in the NaCl-stressed transgenic plants. Taken together, these results suggest that AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress

responses in **Arabidopsis**.

6/3,AB/15 (Item 2 from file: 10)
DIALOG(R)File 10:AGRICOLA
(c) format only 2002 The Dialog Corporation. All rts. reserv.

3417620 20438255 Holding Library: AGL
Plant genes encoding homologues of the SNF1 and **shaggy** protein **kinases**
Kreis, M. Bianchi, M.W.; Ferrant, V.; Le Guen, L.; Thomas, M.; Halford, N.G.; Barker, J.H.A.; Hannappel, U.; Vicente-Carbajosa, J.; Shewry, P.R.
Universite Paris-XI, Orsay, Fr.
[Berlin ; New York : Springer-Verlag, c1986-
NATO ASI series. Series H, Cell biology. 1994. v. 81 p. 453-467.
ISSN: 1010-8793 CODEN: NASBE4
DNAL CALL NO: QH573.N37
Language: English

6/3,AB/16 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

10777729 Genuine Article#: 567BM Number of References: 54
Title: AtSK theta, a plant homologue of SGG/GSK-3 marks developing tissues in **Arabidopsis** thaliana (ABSTRACT AVAILABLE)
Author(s): Tavares R; Vidal J; van Lammeren A; Kreis M (REPRINT)
Corporate Source: Univ Paris 11,CNRS, UMR 8618, Lab Biol Dev Plant,Inst Biotechnol Plantes,F-91405 Orsay//France/ (REPRINT); Univ Paris 11,CNRS, UMR 8618, Lab Biol Dev Plant,Inst Biotechnol Plantes,F-91405 Orsay//France/; Wageningen Univ,Lab Plant Cell Biol,NL-6703 BD Wageningen//Netherlands/
Journal: PLANT MOLECULAR BIOLOGY, 2002, V50, N2 (SEP), P261-271
ISSN: 0167-4412 Publication date: 20020900
Publisher: KLUWER ACADEMIC PUBL, VAN GODEWIJCKSTRAAT 30, 3311 GZ DORDRECHT, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: The **Arabidopsis** thaliana AtSK sub-family of serine threonine protein **kinases** groups 10 homologues of **SHAGGY**/GSK-3. Previous results obtained with different plant members of the **SHAGGY**/GSK-3 family strongly suggest that these proteins are involved in cell differentiation and stress responses. In order to gain further insight into the biological functions of this family in A. thaliana, polyclonal antibodies were raised against specific domains of the AtSKtheta protein. The antibodies were purified and used in immunolocalization studies in various tissues of A. thaliana. Our results show that the protein is located in the cell nuclei of various developing organs. Differential protein localization profiles were found in some of the observed tissues, notably during gametophyte and embryo development. Based on this protein location pattern, and on what is known about the mammalian members of the GSK-3 family, we suggest that AtSKtheta may have a role in the regulation of transcription factors.

6/3,AB/17 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

10607229 Genuine Article#: 546ZU Number of References: 14
Title: Single-embryo RT-PCR assay to study gene expression dynamics during embryogenesis in **Arabidopsis** thaliana (ABSTRACT AVAILABLE)

Author(s): Zou JW; Sun MX (REPRINT) ; Yang HY
Corporate Source: Wuhan Univ,Key Lab MOE Plant Dev Biol,Wuhan 430072/ Peoples R China/ (REPRINT); Wuhan Univ,Key Lab MOE Plant Dev Biol,Wuhan 430072/ Peoples R China/
Journal: PLANT MOLECULAR BIOLOGY REPORTER, 2002, V20, N1 (MAR), P19-26
ISSN: 0735-9640 Publication date: 20020300
Publisher: INT SOC PLANT MOLECULAR BIOLOGY, UNIV GEORGIA, DEPT BIOCHEMISTRY, ATHENS, GA 30602 USA
Language: English Document Type: ARTICLE
Abstract: We have developed a single-embryo RT-PCR protocol for studying gene expression during plant embryogenesis. Four genes, glyceraldhyde-3 phosphate dehydrogenase (GAPC), shoot-meristemless (STM), monopteros (MP), and **shaggy**-like **kinase** etha (ASKeta), from **Arabidopsis** thaliana were used to test the sensitivity and reliability of this method by analyzing the differential signal intensities of their RT-PCR products. The method could detect genes expressed during embryogenesis at a single-embryo level and, therefore, can be used to identify phenotypes. When in vitro, embryogenesis also is used to control the time course of zygote development exactly. The single-embryo RT-PCR protocol becomes a powerful method to survey the dynamics of specific gene expression.

6/3,AB 18 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

10266684 Genuine Article#: 504NE Number of References: 79
Title: The role of protein **kinases** in the regulation of plant growth and development (ABSTRACT AVAILABLE)
Author(s): Laurie S; Halford NG (REPRINT)
Corporate Source: Univ Bristol,Dept Agr Sci, IACR Long Ashton Res Stn,Bristol BS41 9AF/Avon/England/ (REPRINT); Univ Bristol,Dept Agr Sci , IACR Long Ashton Res Stn,Bristol BS41 9AF/Avon/England/
Journal: PLANT GROWTH REGULATION, 2001, V34, N3 (JUL), P253-265
ISSN: 0167-6903 Publication date: 20010700
Publisher: KLUWER ACADEMIC PUBL, VAN GODEWIJCKSTRAAT 30, 3311 GZ DORDRECHT, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: We review the role of protein **kinases** in plant hormone-mediated signalling, nutrient signalling and cell cycle control and in the crosstalk between these different contributors to plant growth regulation. The areas of hormone mediated signalling covered include ABA-mediated responses to osmotic stress, wounding and pathogen attack, as well as ethylene and cytokinin signalling pathways. These areas involve members of several major protein **kinase** families, including the SNF1-related protein **kinase**-2 (SnRK2) subfamily, the calcium-dependent protein **kinase** (CDPK) family, the mitogen activated protein (MAP) **kinase** family, the glycogen synthase **kinase** (GSK)-3 **shaggy** family and the receptor-like protein **kinase** (RPK) family. In the section on nutrient signalling we review the role of SnRK1 protein **kinases** in the global regulation of carbon metabolism, including aspects of sugar sensing and assimilate partitioning, and what is known about nitrogen and sulphur nutrient signalling. In the cell cycle section, we summarise progress in the elucidation of cell cycle control systems in plants and discuss the interaction between cell cycle control and development. We expand further on the hypothesis of crosstalk between different signalling pathways in a separate section in which we discuss evidence for interaction between plant growth regulators and the cell cycle, between different nutrient signalling pathways, between nutrient and cell cycle signalling and between nutrient and ABA signalling.

6/3,AB 19 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

09962873 Genuine Article#: 470HZ Number of References: 9
Title: ULTRACURVATA1, a **SHAGGY**-like **Arabidopsis** gene required for cell elongation (ABSTRACT AVAILABLE)
Author(s): Perez Perez JM; Ponce MR; Micol JL (REPRINT)
Corporate Source: Univ Miguel Hernandez,Div Genet,Campus Elche/Alicante 03202/Spain/ (REPRINT); Univ Miguel Hernandez,Div Genet,Alicante 03202/Spain/; Univ Miguel Hernandez,Inst Bioingn,Alicante 03202/Spain/
Journal: INTERNATIONAL JOURNAL OF DEVELOPMENTAL BIOLOGY, 2001, V45, 1, P S51-S52
ISSN: 0214-6282 Publication date: 20010000
Publisher: U B C PRESS, UNIV BASQUE COUNTRY, EDITORIAL SERVICES, PO BOX 1397, E-48080 BILBAO, SPAIN
Language: English Document Type: ARTICLE
Abstract: To better understand the genetic mechanisms underlying plant leaf development, we have performed a large-scale screening for **Arabidopsis** thaliana mutants to identify those displaying abnormally shaped or sized leaves. One of the stronger mutant phenotypes found was that of the ultracurvata1 (ucu1) mutants, whose vegetative and cauline leaves are spirally rolled downwards and show a reduced expansion along the longitudinal axis, in contrast to wild type leaves, which are flattened organs. We have identified one recessive and two semidominant ucu1 alleles, the most extreme of which cause severe dwarfism and a constitutive photomorphogenic response. Following a map-based strategy, we have cloned the UCU1 gene, which was found to encode an intracellular **kinase** closely related to **SHAGGY**, one of the components of the Wingless/Wnt animal signalling pathway. The responses of ucu1 mutants to exogenous plant hormones and the genetic analyses of double mutants involving ucu1 alleles indicate that UCU1 is a key component in several signalling pathways controlling cell expansion and overall plant growth, including those of auxins and brassinosteroids.

6/3,AB 20 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04112144 Genuine Article#: RF014 Number of References: 52
Title: PETUNIA-HYBRIDA HOMOLOGS OF **SHAGGY** ZESTE-WHITE-3 EXPRESSED IN FEMALE AND MALE REPRODUCTIVE-ORGANS (Abstract Available)
Author(s): DECROOCQFERRANT V; VANWENT J; BIANCHI MW; DEVRIES SC; KREIS M
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES,CNRS,URA 1128,BATIMENT 630/F-91405 ORSAY/FRANCE ; UNIV PARIS 11,INST BIOTECHNOL PLANTES,CNRS,URA 1128/F-91405 ORSAY/FRANCE/; AGR UNIV WAGENINGEN,DEPT PLANT CYTOL & MORPHOL/6703 BD WAGENINGEN/NETHERLANDS/ ; AGR UNIV WAGENINGEN,DEPT MOLEC BIOL 6703 HA WAGENINGEN//NETHERLANDS/
Journal: PLANT JOURNAL, 1995, V7, N6 (JUN), P897-911
ISSN: 0960 7412
Language: ENGLISH Document Type: ARTICLE
Abstract: Petunia hybrida ovule-specific cDNA libraries were screened for genes encoding homologues of protein **kinases** known to be involved in developmental processes. Two cDNAs, PSK4 and PSK6 (Petunia hybrida **shaggy** related protein **kinase**), homologous to GSK-3 from rat, MDS1 from yeast and to the segment polarity gene **shaggy** /zeste white 3 (sgg/zw3) from Drosophila were characterized in detail. Southern blot analysis showed that the PSK4 and PSK6 genes belong to a small multigene family in P. hybrida. The PSK4 and PSK6 proteins, which are 70% identical to sgg/zw3 and its functional homologue GSK-3 over the protein **kinase** catalytic domain and 85% identical to MDS1,

represent two different subgroups of protein **kinases**. RNA gel blot and RT-PCR analyses revealed that the PSK4 gene is expressed during the vegetative phase and the female reproductive phase of development and the PSK6 gene predominantly during the male and female reproductive phases. In situ hybridization on developing flower buds confirmed that PSK4 is expressed throughout the different developmental stages from ovule primordium formation until embryo sac maturation, while PSK6 showed expression during anther cell differentiation and at pollen maturity, and an expression pattern similar to PSK4 in the female reproductive organs. The results also revealed transcripts of a PSK gene in embryos at the globular stage.

6/3,AB/21 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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02713520 5377769
The UCU1 **Arabidopsis** Gene Encodes a **SHAGGY**/GSK3-like **Kinase** Required for Cell Expansion along the Proximodistal Axis
Perez Perez, J.M.; Ponce, M.R.; Micol, J.L.
Division de Genetica and Instituto de Bioingenieria, Universidad Miguel Hernandez, Campus de Elche, 03202 Elche, Alicante, Spain
Developmental Biology vol. 242, no. 2, pp. 161-173 (2002)
ISSN: 0012-1606
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Genetics Abstracts

Most signal transduction pathways central to development are not shared by plants and animals. Such is the case of the Wingless/Wnt signaling pathway, whose components play key roles in metazoan pattern formation and tumorigenesis, but are absent in plants, with the exception of **SHAGGY**/GSK3, a cytoplasmic protein **kinase** represented in the genome of **Arabidopsis** thaliana by a family of 10 AtSK genes for which mutational evidence is scarce. Here, we describe the characterization of mutant alleles of the **Arabidopsis** ULTRACURVATA1 (UCU1) gene, the two strongest of which dramatically reduce cell expansion along the proximodistal axis, dwarfing the mutant plants, whose cells expand properly across but not along most organs. Proximodistal expansion of adaxial (dorsal) and abaxial (ventral) leaf cells exhibits a differential dependence on UCU1 function, as suggested by the leaves of ucu1 mutants, which are rolled spirally downward in a circinate manner. We have positionally cloned the UCU1 gene, which encodes an AtSK protein involved in the cross-talk between auxin and brassinosteroid signaling pathways, as indicated by the responses of ucu1 mutants to plant hormones and the phenotypes of double mutants involving ucu1 alleles.

6/3,AB/22 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02359959 4495739
Characteriztion of three novel members of the **Arabidopsis** **SHAGGY**-related protein **kinase** (ASK) multigene family
Dornelas, M.C.; Wittich, P.; von Recklinghausen, I.; van Lammeren, A.; Kreis, M.
Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris-Sud, Batiment 630, 91405 Orsay Cedex, France
Plant Molecular Biology vol. 39, no. 1, pp. 137-147 (1999)
ISSN: 0167-4412
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Genetics Abstracts; Biochemistry Abstracts 2: Nucleic Acids

In this paper we report the characterization of three novel members of the **Arabidopsis shaggy**-related protein **kinase** (ASK) multigene family, named ASKdzeta (ASK), ASKetha (ASK eta) and ASKiota (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to **SHAGGY** (SGG) and glycogen synthase **kinase**-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein **kinases** demonstrated a clear distinction between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these **kinases**. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASK\g?\ is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha , ASK gamma and ASK iota in developing embryos.

6/3,AB/23 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

15494275 PASCAL No.: 02-0189640
Regulation of brassinosteroid signaling by a GSK3/**SHAGGY**-like **kinase**
JIANMING LI; KYOUNG HEE NAM
Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI 48109-1048, United States
Journal: Science : (Washington, D.C.), 2002, 295 (5558) 1299-1301
Language: English
GSK3/**SHAGGY** is a highly conserved serine/threonine **kinase** implicated in many signaling pathways in eukaryotes. Although many GSK3/**SHAGGY**-like **kinases** have been identified in plants, little is known about their functions in plant growth and development. Here we show that the **Arabidopsis** BRASSINOSTEROID-INSENSITIVE 2 (BIN2) gene encodes a GSK3/**SHAGGY**-like **kinase**. Gain-of-function mutations within its coding sequence or its overexpression inhibit brassinosteroid (BR) signaling, resulting in plants that resemble BR-deficient and BR-response mutants. In contrast, reduced BIN2 expression via cosuppression partially rescues a weak BR-signaling mutation. Thus, BIN2 acts as a negative regulator to control steroid signaling in plants.

6/3,AB/24 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal

15434165 PASCAL No.: 02-0178682
Contribution a la caracterisation de la sous-famille des proteines serine/threonine **kinases** du type **SHAGGY**/GSK-3 chez **Arabidopsis** thaliana
(Contribution to the characterization of the **Arabidopsis** thaliana **SHAGGY**/GSK-3 subfamily of serine/threonine proteine **kinases**)
TAVARES Raquel; FREIS Martin, dir

Universite de Paris 11, Orsay, France
Univ.: Universite de Paris 11, Orsay, FRA Degree: Th. doct.
2000-12; 2000 232 p.
Language: French Summary Language: French; English

Chez les animaux, les proteines serine/threonine **kinases** de la famille **SHAGGY** /GSK-3 sont impliquees dans une grande variete de processus biologiques, comme la regulation de l'insuline et la determination de la destinee et de la proliferation cellulaires. Ce travail de these avait comme objectif de contribuer a l'elucidation des roles biologiques de ces proteines chez les plantes, plus particulierement a travers l'identification et l'etude d'un sous-groupe de cette famille chez **Arabidopsis**. L'analyse des sequences des genes AtSK (**Arabidopsis** thaliana **SHAGGY**-like **Kinases**) du groupe III a permis de completer les etudes concernant l'organisation et l'evolution de la famille **shaggy** /GSK-3 chez les plantes. Par ailleurs, la caracterisation de l'environnement genomique des differents paralogues nous a amenes a la caracterisation de la structure et de l'evolution de quatre autres familles multigeniques chez **Arabidopsis** . Des etudes d'expression des genes AtSK du groupe III ont ete realisees utilisant des techniques de RT-PCR et de PCR sur des banques d'ADNc. L'imunolocalisation de quatre AtSK a egalement ete effectuee, sur des extraits proteiques et sur des coupes, en utilisant des anticorps specifiques. La localisation intracellulaire de la proteine AtSK THETA a notamment ete determinee. Enfin, la connaissance des sequences genomiques de la totalite de la famille AtSK nous a permis de tester les fonctions biologiques des differents paralogues par des techniques de genetique inverse. La modification in vivo de l'expression des genes AtSK du groupe III a ete entreprise, par le biais de la production de plantes d'**Arabidopsis** comportant des sequences antisens specifiques. Nous avons utilise un systeme de transactivation de l'expression de la sequence antisens dans la descendance de deux lignees, une lignee antisens et une lignee activatrice, presentant un phenotype sauvage.

6/3,AB/25 (Item 3 from file: 144
DIALOG(R)File 144:Pascal

15255167 PASCAL No.: 01-0424400

Constitutive over-expression of AtGSK1 induces NaCl stress responses in the absence of NaCl stress and results in enhanced NaCl tolerance in **Arabidopsis**

HAI LAN PIAO; JEONG HWA LIM; SOO JIN KIM; CHEONG Gang-Won; HWANG Inhwan
Center for Plant Intracellular Trafficking, Pohang University of Science and Technology, Pohang, 790-784, Korea, Republic of; Department of Biochemistry, Gyeongsang National University, Chinju, 660-701, Korea, Republic of; Division of Molecular and Life Sciences, Pohang University of Science and Technology, Pohang, 790-784, Korea, Republic of

Journal: Plant journal, 2001, 27 (4) 305-314
Language: English

GSK3/**shaggy**-like protein **kinases** have been shown to play diverse roles in development and signal transduction pathways in various organisms. An **Arabidopsis** homologue of GSK3/**shaggy**-like **kinase** , AtGSK1, has been shown to be involved in NaCl stress responses. In order to further clarify the role of AtGSK1 in NaCl stress responses in plants, we generated transgenic **Arabidopsis** plants that over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl stress when assayed either as whole plants or by measurement of root growth on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of NaCl stress showed phenotypic changes, such as accumulation of anthocyanin, that were similar to those observed in wild-type plants under NaCl stress. Transgenic plants accumulated 30-50% more Na SUP + than did wild-type

plants when subjected to NaCl stress, and Ca SUP 2 SUP + content was increased by 15-30% in the transgenic plants regardless of the NaCl stress level. Northern blotting revealed that AtGSK1 over-expression induced expression of the NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl stress. In addition, AtCBL1 and AtCP1 were super-induced in the NaCl-stressed transgenic plants. Taken together, these results suggest that AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress responses in **Arabidopsis**.

6 3,AB/26 (Item 4 from file: 144)
DIALOG(R)File 144:Pascal
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14249399 PASCAL No.: 99-0452372
Caracterisation d'homologues de la proteine **kinase SHAGGY** chez **Arabidopsis** thaliana et leur role biologique pendant le developpement
(Characterization of **Arabidopsis** thaliana homologues of **SHAGGY** protein **kinase** and their biological role during development)
DORNELAS Marcelo; KREIS Martin, dir
Universite de Paris 11, Orsay, Francee
Univ.: Universite de Paris 11, Orsay, FRA Degree: Th. doct.
1999-05; 1999 182 p.
Language: French Summary Language: French; English
Trois nouveaux membres de la famille multigenique ASK (pour **Arabidopsis SHAGGY** - related protein **kinases**) nommes ASKdzeta (ASK zeta), ASKetha (ASK eta) et ASKiota (ASK iota), ont ete identifies chez **Arabidopsis** thaliana. Les genes ASK sont des homologues vegetaux du gene **SHAGGY** (SGG) chez la Drosophila, appartenant a la sous-famille GSK-3 des proteines **kinases**. Dans un premier temps, la comparaison des sequences d'acides amines des proteines **kinases** de la sous-famille GSK-3 a permis l'identification de trois groupes, evolutivement conserves, d'homologues vegetaux de SGG. La comparaison des sequences nucleotidiques des genes de la famille ASK a permis la proposition d'un modele d'evolution de cette famille multigenique. Par la suite, l'expression des genes ASK des groupes I et II a ete etudiee pendant le developpement d'**Arabidopsis** utilisant la technique d'hybridation in situ. Des plantes transgeniques contenant des constructions antisens des genes ASK des groupes I et II ont ete obtenues. L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les proteines ASK pendant le developpement floral et embryonnaire d'**Arabidopsis**.

6 3,AB/27 (Item 5 from file: 144)
DIALOG(R)File 144:Pascal
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14074777 PASCAL No.: 99-0267163
An **Arabidopsis** GSK3/**shaggy**-like gene that complements yeast salt stress-sensitive mutants is induced by NaCl and abscisic acid
BAI LAN PIAO; KYEONG TAE PIH; JEONG HWA LIM; SHIN GENE KANG; JING BO JIN; SUNG HEE KIM; HWANG I
Department of Molecular Biology, Gyeongsang National University, Chinju, 660-701, Korea, Republic of; Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Chinju, 660-701, Korea, Republic of
Journal: Plant physiology : (Bethesda), 1999, 119 (4) 1527-1534

Language: English

GSK3/**shaggy**-like genes encode **kinases** that are involved in a variety of biological processes. By functional complementation of the yeast calcineurin mutant strain DHT22-1a with a NaCl stress-sensitive phenotype, we isolated the **Arabidopsis** cDNA AtGSK1, which encodes a GSK3/**shaggy**-like protein **kinase**. AtGSK1 rescued the yeast calcineurin mutant cells from the effects of high NaCl. Also, the AtGSK1 gene turned on the transcription of the NaCl stress-inducible PMR2A gene in the calcineurin mutant cells under NaCl stress. To further define the role of AtGSK1 in the yeast cells we introduced a deletion mutation at the MCK1 gene, a yeast homolog of GSK3, and examined the phenotype of the mutant. The mck1 mutant exhibited a NaCl stress-sensitive phenotype that was rescued by AtGSK1. Also, constitutive expression of MCK1 complemented the NaCl-sensitive phenotype of the calcineurin mutants. Therefore, these results suggest that Mck1 p is involved in the NaCl stress signaling in yeast and that AtGSK1 may functionally replace Mck1p in the NaCl stress response in the calcineurin mutant. To investigate the biological function of AtGSK1 in **Arabidopsis** we examined the expression of AtGSK1. Northern-blot analysis revealed that the expression is differentially regulated in various tissues with a high level expression in flower tissues. In addition, the AtGSK1 expression was induced by NaCl and exogenously applied ABA but not by KCl. Taken together, these results suggest that AtGSK1 is involved in the osmotic stress response in **Arabidopsis**.

6/3,AB/28 (Item 6 from file: 144)
DIALOG(R)File 144:Pascal

11433753 PASCAL No.: 94-0267915

Isolement et caracterisation d'homologues de la proteine **kinase** **shaggy**/GSK-3 chez **Arabidopsis** thaliana et identification d'un gene correspondant chez Saccharomyces cerevisiae

(Isolation and characterization of **Arabidopsis** thaliana homologs of the **shaggy**/gsk-3 protein **kinase** and identification of a corresponding gene in Saccharomyces cerevisiae)

BIANCHI Michele; KREIS Martin, dir

Universite de Paris 11, Francee

Univ.: Universite de Paris 11, FRA Degree: Th. doct.

1993-09; 1993 155 p.

Language: French Summary Language: French; English

Les proteines **kinases** (PKs) sont les composants centraux du systeme cybernetique des cellules eucaryotes. L'identification d'homologues de PKs conservees au cours de l'evolution peut constituer une approche complementaire aux techniques genetiques pour l'etude de voies de transduction importantes chez les plantes. Dans un premier temps, une approche de PCR (polymerase chain reaction) a permis d'identifier, chez **Arabidopsis** thaliana, une famille de genes apparentes a (1) MCK1 (meiosis and centromere regulatory **kinase**) de Saccharomyces cerevisiae; (2) **shaggy**/zeste-white 3, impliquee dans le developpement de Drosophila melanogaster; (3) le gene codant la glycogen synthase **kinase**-3 (GSK-3, regulateur du facteur transcriptionnel c-Jun) de mammiferes. Par la suite, la caracterisation de deux ADNc, ASK-alpha et ASK-gamma (**Arabidopsis** **shaggy**-related protein **kinase**), a permis de mettre en evidence une identite de 70%, au niveau du domaine catalytique, entre les proteines ASK et **shaggy**/GSK-3 dont ils representent donc les homologues vegetaux. L'activite **kinase** ainsi qu'une autophosphorylation sur des residus threonine, serine et, en plus faible quantite, tyrosine, ont pu etre demontrees apres production des proteines ASK dans E. coli. Par ailleurs, le niveau relativement faible d'identite avec MCK1 (40%) a mene a la recherche puis a l'isolement d'un

deuxieme gene de S. cerevisiae: ScGSK-3, dont le produit putatif est identique a 60%, au niveau du domaine catalytique, avec GSK-3, **shaggy** et les proteines ASK. Une analyse de phylogenie moleculaire a suggere que ScGSK-3 code le veritable homologue de GSK-3 et **shaggy**, alors que MCK1 serait originaire d'un evenement de duplication specifique du lignage de S. cerevisiae. L'etude simultanee des PKs de la famille GSK-3 dans differents organismes devrait fournir une aide importante a la comprehension des fonctions biochimiques et biologiques des proteines ASK chez les plantes superieures
?

```
Set      Items   Description
S1        7347   ARABIDOPSIS AND KINAS?
S2          90   S1 AND SHAGGY
S3          55   S1 AND ASK
S4           0   S1 AND DZETA
S5          21   S1 AND ZETA
S6          28   RD S2 (unique items)
? rd a3
>>>'A3' is not a correct set number.
? rd s3
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...examined 50 records  (50)
>>>Record 266:276026 ignored; incomplete bibliographic data, not retained -
in RD set
...completed examining records
      S7      22  RD S3 (unique items)
? s s7 not s6
              22  S7
              28  S6
      S8      15  S7 NOT S6
? t s8/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

 8/3,AB/1      (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10579927   20098709   PMID: 10631245
  Identification by large-scale screening of phytochrome-regulated genes in
etiolated seedlings of Arabidopsis using a fluorescent differential
display technique.
  Kuno N; Muramatsu T; Hamazato F; Furuya M
  Hitachi Advanced Research Laboratory, Hatoyama, Saitama 350-0395, Japan.
  Plant physiology (UNITED STATES) Jan 2000, 122 (1) p15-24, ISSN
0032-0889 Journal Code: 0401224
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Phytochrome A (PhyA)-regulated genes in 6-d-old etiolated seedlings of
Arabidopsis Landsberg erecta were identified by fluorescent
differential display. To screen for PhyA-regulated genes, mRNA fingerprints
of the wild type and the phyA-201 mutant were compared from samples
prepared 4 h after far-red light irradiation. Approximately 30,000 bands of
cDNA were displayed by fluorescent differential display, and 24
differentially expressed bands were observed. Sequence analysis revealed
that they represent 20 distinct genes. Among them, 15 genes were confirmed
as PhyA regulated by northern-blot (or reverse transcription-polymerase
chain reaction) analysis. Thirteen up-regulated genes included 12 known
genes that encode nine photosynthetic proteins, two enzymes involved in the
biosynthesis of chlorophyll, one DNA damage repair/toleration-related
protein, and one unknown gene. Two down-regulated genes were identified as
encoding a xyloglucan endotransglycosylase-related protein and a novel
member of the ASK protein kinase family. In the phyA-201 mutant
and the phyA-201phyB-1 double mutant, expression of all of these genes was
photoreversibly up- or down-regulated by type II phytochromes. The results
indicate that modes of photoperception differ between PhyA and PhyB, but
that both types of phytochromes have overlapping effects on the
photoregulation of gene expression.
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8/3,AB/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06560880 Genuine Article#: 300TZ Number of References: 51
Title: **Arabidopsis** thaliana SHAGGY-related protein **kinases** (AtSK11 and 12) function in perianth and gynoecium development (ABSTRACT AVAILABLE)
Author(s): Dornelas MC; vanLammeren AAM; Kreis M (REPRINT)
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618, BATIMENT 630,F-91405 ORSAY,/FRANCE/ (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618,F-91405 ORSAY//FRANCE/; AGR UNIV WAGENINGEN,LAB EXPT PLANT MORPHOL & CELL BIOL/NL-6703 BD WAGENINGEN,/NETHERLANDS/
Journal: PLANT JOURNAL, 2000, V21, N5 MAR, P419-429
ISSN: 0960-7412 Publication date: 20000300
Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND
Language: English Document Type: ARTICLE
Abstract: In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein **kinase** genes AtSK11(**ASK** alpha) and AtSK12(**ASK** gamma). The AtSK genes are plant homologues of the Drosophila shaggy (SGG) gene and the mammalian Glycogen-Synthase **Kinase**-3 (GSK-3). The SGG protein **kinase** is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(**ASK** alpha) and AtSK12(**ASK** gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(**ASK** alpha) and AtSK12(**ASK** gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(**ASK** alpha) and AtSK12(**ASK** gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

8/3,AB/3 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06509422 Genuine Article#: YY117 Number of References: 44
Title: A state-independent interaction between ligand and a conserved arginine residue in cyclic nucleotide-gated channels reveals a functional polarity of the cyclic nucleotide binding site (ABSTRACT AVAILABLE)
Author(s): Tibbs GR (REPRINT) ; Liu DT; Leypold BG; Sigelbaum SA
Corporate Source: COLUMBIA UNIV,DEPT PHARMACOL, CTR NEUROBIOL & BEHAV, 722 W 168TH ST,NEW YORK,/NY/10032 (REPRINT); COLUMBIA UNIV,HOWARD HUGHES MED INST,/NEW YORK/,NY/10032
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N8 (FEB 20), P4497-4505
ISSN: 0021-9258 Publication date: 19980220
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: Activation of cyclic nucleotide-gated channels is thought to

involve two distinct steps: a recognition event in which a ligand binds to the channel and a conformational change that both opens the channel and increases the affinity of the channel for an agonist, Sequence similarity with the cyclic nucleotide binding sites of cAMP- and cGMP-dependent protein **kinases** and the bacterial catabolite activating protein (CAP) suggests that the channel ligand binding site consists of a beta-roll and three alpha-helices, Recent evidence has demonstrated that the third (or C) alpha-helix moves relative to the agonist upon channel activation, forming additional favorable contacts with the purine ring, Here we **ask** if channel activation also involves structural changes in the beta-roll by investigating the contribution of a conserved arginine residue that, in CAP and the **kinases**, forms an important ionic interaction with the cyclized phosphate of the bound ligand, Mutations that conserve, neutralize, or reverse the charge on this arginine decreased the apparent affinity for ligand over four orders of magnitude but had little effect on the ability of bound ligand to open the channel, These data indicate that the cyclized phosphate of the nucleotide approaches to within 2-4 Angstrom of the arginine, forming a favorable ionic bond that is largely unaltered upon activation, Thus, the binding site appears to be polarized into two distinct structural and functional domains: the beta-roll stabilizes the ligand in a state-independent manner, whereas the C-helix selectively stabilizes the ligand in the open state of the channel. It is likely that these distinct contributions of the nucleotide/C-helix and nucleotide/beta-roll interactions may also be a general feature of the mechanism of activation of other cyclic nucleotide-binding proteins.

8/3,AB/4 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05260701 Genuine Article#: VL534 Number of References: 202
Title: THE GENES OF PLANT SIGNAL-TRANSDUCTION (Abstract Available)
Author(s): REDHEAD CR; PALME K
Corporate Source: MAX PLANCK GESELL,MAX DELBRUCK LAB,CARL VON LINNE WEG 10 D-50829 COLOGNE/,GERMANY/
Journal: CRITICAL REVIEWS IN PLANT SCIENCES, 1996, V15, N5-6, P425-454
ISSN: 0735-2689
Language: ENGLISH Document Type: REVIEW
Abstract: Due to the enormous importance of plants as a source of both food and raw materials, an understanding of the control of their growth and development is imperative. Basic to this understanding is the identification of the genes that enable the plant to adapt to its environment while at the same time adhering to its basic developmental plan. The aims of this review are first to briefly summarize the various approaches that have been used to identify these plant signaling genes and second to give an overview of the genes that have been cloned so far and what these genes may tell us about the nature of signal transduction in plants. The advent of modern molecular biology and molecular genetics has revolutionized our ability to unravel the complexities of plant signal transduction pathways. A whole battery of techniques are now available to identify the genes that control the plants development and ability to adapt to its environment.(65) Each technique has its own strengths and weaknesses and must be carefully selected by the researcher according to the question that he or she would like to **ask**.

8/3,AB/5 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03433854 CAB Accession Number: 971609343

Differential expression of two functional serine/threonine protein **kinases** from soyabean that have an unusual acidic domain at the carboxy terminus.

Yoon, H. W.; Kim, M. C.; Shin, P. G.; Kim, J. S.; Kim, C. Y.; Lee, S. Y. ; Hwang, I.; Bahk, J. D.; Hong, J. C.; Han, C.; Cho, M. J.

Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Chinju 660-701, Korea Republic.

Molecular and General Genetics vol. 255 (4): p.359-371

Publication Year: 1997

ISSN: 0026-8925 --

Language: English

Document Type: Journal article

Two soyabean cDNA clones, SPK3 and SPK4, encoding putative protein **kinases** were isolated and characterized (GenBank accession numbers L19361 and L38855, respectively). Both cDNAs encoded approximately 40 kDa serine/threonine **kinases** with unusual stretches of acidic amino acids in their carboxy-terminal regions, which are highly homologous to the wheat PKABA1 and **Arabidopsis ASK kinases**. These **kinases** are encoded by one- or two-copy genes in the soyabean genome. Notably, SPK3 and SPK4 showed different patterns of expression in various soyabean tissues. SPK3 was highly expressed in dividing and elongating tissues of young seedlings, but relatively weakly in tissues of mature plants. In contrast, SPK4 showed relatively high and constitutive expression in all the tissues examined except for leaf tissues of mature plants. Although various stressors, such as dehydration and high salinity, increased the expression of both genes, the induction kinetics were different. The two genes also differed in their response to abscisic acid (ABA). SPK3 was induced but SPK4 was not affected by exogenously supplied abscisic acid. In accordance with these expression data, analysis of the activity of a chimaeric SPK3 promoter:: beta -glucuronidase (GUS) reporter gene by transient expression in tobacco leaves confirmed the inducibility of SPK3 by salt and ABA. Polyclonal antibodies raised against a recombinant SPK4 protein produced in Escherichia coli specifically recognized both recombinant SPK3 and SPK4 proteins. **Kinase** assays using affinity-purified SPK4/antibody complexes with crude soyabean extracts as substrate identified specific phosphorylation of two 41 and 170 kDa soyabean proteins that were phosphorylated on serine residues. Taken together, these results suggested that SPK3, and/or SPK4 are functional serine protein **kinase**(s). Furthermore, SPK3 and SPK4 may play different roles in the transduction of various environmental stresses. 47 ref.

8/3,AB/6 (Item 1 from file: 98)

04600393 H.W. WILSON RECORD NUMBER: BGSA01000393

The ecology and physiology of viviparous and recalcitrant seeds.

Farnsworth, Elizabeth

Annual Review of Ecology and Systematics v. 31 (2000) p. 107-38

SPECIAL FEATURES: bibl graph il tab ISSN: 0066-4162

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 12647

ABSTRACT: Understanding seed physiology is central to reconstructing how angiosperms have evolved, to characterizing dormancy and germination regimes shared by suites of species, and to devising sound strategies for seed bank conservation, agriculture, and forestry. While species with dormant seeds have received the lion's share of attention, hundreds of plant species exhibit no seed dormancy and germinate either viviparously on the parent plant or shortly after release. Embryos of these recalcitrant

and viviparous species cannot tolerate the maturation drying that is usually prerequisite to dormancy; such desiccation intolerance creates challenges for storing and preserving such embryos. I review the physiology, morphology, and ecology of these desiccation-intolerant, nondormant lineages. Differences in the production and function of plant hormones are implicated in the occurrence of recalcitrance and vivipary in plant families. Plant hormones are key regulators of seed physiology and simultaneously coordinate responses of the seedling and mature plant to their environment. Desiccation-intolerant embryos occur most commonly among species of wet or flooded environments and have evolved multiple times in disparate lineages. Natural selection in wetland environments simply may not eliminate these seed types or may select for changes in hormone physiology that simultaneously affect both maternal and embryonic tissues. Integrative data from ecological, genetic, and physiological studies are needed to elucidate evolutionary origins and maintenance of reproductive strategies in organisms. Reprinted by permission of the publisher.

8/3,AB/7 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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94862830 H.W. WILSON RECORD NUMBER: BGSA00112830
Genomic imprinting and environmental disease susceptibility.
AUGMENTED TITLE: workshop summary
Jirtle, Randy L
Sander, Miriam; Barrett, J. Carl
Environmental Health Perspectives (Environ Health Perspect) v. 108 no3 (Mar. 2000) p. 271-8
SPECIAL FEATURES: bibl ISSN: 0091-6765
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8781

ABSTRACT: Genomic imprinting is one of the most intriguing subtleties of modern genetics. The term "imprinting" refers to parent-of-origin-dependent gene expression. The presence of imprinted genes can cause cells with a full parental complement of functional autosomal genes to specifically express one allele but not the other, resulting in monoallelic expression of the imprinted loci. Genomic imprinting plays a critical role in fetal growth and behavioral development, and it is regulated by DNA methylation and chromatin structure. This paper summarizes the Genomic Imprinting and Environmental Disease Susceptibility Conference held 8-10 October 1998 at Duke University, Durham, North Carolina. The conference focused on the importance of genomic imprinting in determining susceptibility to environmentally induced diseases. Conference topics included rationales for imprinting: parental antagonism and speciation; methods for imprinted gene identification: allelic message display and monochromosomal mouse/human hybrids; properties of the imprinted gene cluster human 11p15.5 and mouse distal 7; the epigenetics of X-chromosome inactivation; variability in imprinting: imprint erasure, non-Mendelian inheritance ratios, and polymorphic imprinting; imprinting and behavior: genetics of bipolar disorder, imprinting in Turner syndrome, and imprinting in brain development and social behavior; and aberrant methylation: methylation and chromatin structure, methylation and estrogen exposure, methylation of tumor suppressor genes, and cancer susceptibility. Environmental factors are capable of causing epigenetic changes in DNA that can potentially alter imprint gene expression and that can result in genetic diseases including cancer and behavioral disorders. Understanding the contribution of imprinting to the regulation of gene expression will be an important step in evaluating environmental influences on human health and disease. Reprinted by permission of the publisher.

8/3,AB/8 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04272504 H.W. WILSON RECORD NUMBER: BGSA00022504
Swinging arms and swinging domains in multifunctional enzymes: catalytic machines for multistep reactions.
Perham, Richard N
Annual Review of Biochemistry v. 69 (2000) p. 961-1004
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 19859

ABSTRACT: Multistep chemical reactions are increasingly seen as important in a growing number of complex biotransformations. Covalently attached prosthetic groups or swinging arms, and their associated protein domains, are essential to the mechanisms of active-site coupling and substrate channeling in a number of the multifunctional enzyme systems responsible. The protein domains, for which the posttranslational machinery in the cell is highly specific, are crucially important, contributing to the processes of molecular recognition that define and protect the substrates and the catalytic intermediates. The domains have novel folds and move by virtue of conformationally flexible linker regions that tether them to other components of their respective multienzyme complexes. Structural and mechanistic imperatives are becoming apparent as the assembly pathways and the coupling of multistep reactions catalyzed by these dauntingly complex molecular machines are unraveled. Reprinted by permission of the publisher.

8/3,AB/9 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04269830 H.W. WILSON RECORD NUMBER: BGSA00019830
Stomatal patterning in angiosperms.
Croxdale, Judith L
American Journal of Botany (Am J Bot) v. 87 no8 (Aug. 2000) p. 1069-80
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11339

ABSTRACT: My thesis is that understanding stomatal patterning requires a holistic perspective. Since stomata are structures critical to the survival of terrestrial plants, they need to be viewed in relation to their function and their interface with other structural components. With this outlook, I begin by discussing pattern types, means of measuring them, advantages of each type of measurement, and then present patterning from evolutionary, physiological, ecological, and organ views. I suggest areas where I believe profitable studies might enable us to better understand stomatal patterning. The final sections of the paper review stomatal patterning on angiosperm leaves and present a theory of patterning. With the abundance of molecular information, and coming genomic sequences and new tools, an opportunity exists to dissect the process of how cells are selected to become different from their neighbors and assume a fate critical to plant survival. Understanding this biological process at the molecular level requires comprehending the broad base on which stomatal patterning rests. Reprinted by permission of the publisher.

8/3,AB/10 (Item 5 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04250985 H.W. WILSON RECORD NUMBER: BGSA00000985
Analysis of selection on enzyme polymorphisms.
Eanes, Walter F
Annual Review of Ecology and Systematics v. 30 (1999) p. 301-26
SPECIAL FEATURES: bibl ISSN: 0066-4162
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12061

ABSTRACT: The role of amino acid polymorphisms in adaptive evolution is considered. Studies of model systems indicate that selection may act on enzyme polymorphisms in metabolic genes. In addition, there is evidence that regulatory changes are superimposed on structural changes. Although metabolic responses to selection are multilocus in nature, all enzymes in contributing pathways may not be equal. Further study is needed to determine the rule for these inequalities.

8/3,AB/11 (Item 6 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04050515 H.W. WILSON RECORD NUMBER: BGSA99050515
Circadian programs in cyanobacteria: adaptiveness and mechanism.
AUGMENTED TITLE: review
Johnson, Carl Hirschie
Golden, Susan S
Annual Review of Microbiology v. 53 (1999) p. 389-409
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8362

ABSTRACT: At least one group of prokaryotes is known to have circadian regulation of cellular activities--the cyanobacteria. Their "biological clock" orchestrates cellular events to occur in an optimal temporal program, and it can keep track of circadian time even when the cells are dividing more rapidly than once per day. Growth competition experiments demonstrate that the fitness of cyanobacteria is enhanced when the circadian period matches the period of the environmental cycle. Three genes have been identified that specifically affect circadian phenotypes. These genes, kaiA, kaiB, and kaiC, are adjacent to each other on the chromosome, thus forming a clock gene cluster. The clock gene products appear to interact with each other and form an autoregulatory feedback loop.
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8/3,AB/12 (Item 7 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04045911 H.W. WILSON RECORD NUMBER: BGSI99045911
MCM proteins in DNA replication.
Tye, Bik K
Annual Review of Biochemistry v. 68 (1999) p. 649-86
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 17809

ABSTRACT: The MCM proteins are essential replication initiation factors originally identified as proteins required for minichromosome maintenance in Saccharomyces cerevisiae. The best known among them are a family of six

structurally related proteins, MCM2-7, which are evolutionally conserved in all eukaryotes. The MCM2-7 proteins form a hexameric complex. This complex is a key component of the prereplication complex that assembles at replication origins during early G1 phase. New evidence suggests that the MCM2-7 proteins may be involved not only in the initiation but also in the elongation of DNA replication. Orchestration of the functional interactions between the MCM2-7 proteins and other components of the prereplication complex by cell cycle-dependent protein **kinases** results in initiation of DNA synthesis once every cell cycle. Reprinted by permission of the publisher.

8/3,AB/13 (Item 8 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04014401 H.W. WILSON RECORD NUMBER: BGSI99014401
Heat-shock proteins, molecular chaperones, and the stress response: evolutionary and ecological physiology.
AUGMENTED TITLE: review
Feder, Martin E
Hofmann, Gretchen E
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82
SPECIAL FEATURES: bibl il ISSN: 0066-4278
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual Review of Physiology, Volume 61, 1999, by Annual Reviews Inc. (http://www.annurev.org).

8/3,AB/14 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03506131 H.W. WILSON RECORD NUMBER: BGSI97006131
Genetic and molecular analysis of circadian rhythms.
Dunlap, Jay C
Annual Review of Genetics (Annu Rev Genet) v. 30 ('96) p. 579-601
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11723

ABSTRACT: The genetic and molecular bases of circadian rhythms are reviewed. Most of the current evidence suggests that biological clocks are based on negative feedback loops involving the rhythmic expression of proteins that shut off their own synthesis. The 2 best understood circadian systems are those of Neurospora (frequency (frq) gene) and Drosophila (period (per) and timeless genes). Most organisms appear to use a day-phased oscillator similar to that of Neurospora rather than the night-phased system of Drosophila. Both frq and per are widely conserved within their corresponding phylogenetic classes. Studies of the molecular basis of biological clocks have focused on 3 main areas: the underlying biochemical and genetic bases of oscillators, the synchronization of the oscillator with the geophysical cycles of the external world, and the means by which the clock alters the behavior of the cell and the organism.

8/3,AB/15 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
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0230234 DBA Accession No.: 99-00335
APS-**kinase** from **Arabidopsis** thaliana: genomic organization, expression, and kinetic analysis of the recombinant enzyme - recombinant adenylylsulfate-**kinase** expression and characterization
AUTHOR: Lee S; +Leustek T
CORPORATE AFFILIATE: Univ.New-Jersey-State
CORPORATE SOURCE: Biotech Center and Plant Science Department, Rutgers University, 59 Dudley Road, New Brunswick, NJ 08901-8250, USA. email:leustek@aesop.rutgers.edu
JOURNAL: Biochem.Biophys.Res.Commun. (247, 1, 171-75) 1998
ISSN: 0006-291X CODEN: BBRCA9
LANGUAGE: English
ABSTRACT: To determine whether adenylylsulfate-**kinase** (**ASK**, EC-2.7.1.25) in plants differs kinetically from that in Escherichia coli and Penicillium chrysogenum, a cDNA encoding **ASK** was cloned from **Arabidopsis** thaliana by functional complementation of a met14 mutant strain of Saccharomyces cerevisiae. **ASK** could also complement an Escherichia coli cysC strain. **ASK** was expressed as a recombinant protein by cloning the cDNA as a 980 bp BglII-BamHIH fragment into plasmid pGEX-2T and separately into plasmid pMAL-c2, followed by transformation of E. coli JM81A. The properties of recombinant **ASK** are described. The gene encoding **ASK** was shown to be composed of 7 exons, interrupted by 6 introns. Recombinant **ASK** was able to enter isolated intact chloroplasts and showed maximum activity at 10 uM substrate with 5 mM ATP, but was inhibited by more than 10 uM adenylylsulfate. The enzyme had a Vmax of 1.2 umol/min.mg at 25 deg and pH 8, and a Km value of 3.6 uM adenylylsulfate and 1.8 mM ATP. (25 ref)
?

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Set     Items   Description
S1       7347   ARABIDOPSIS AND KINAS?
S2         90   S1 AND SHAGGY
S3         55   S1 AND ASK
S4          0   S1 AND DZETA
S5         21   S1 AND ZETA
S6         28   RD S2 (unique items)
S7         22   RD S3 (unique items)
S8         15   S7 NOT S6
? rd s5
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records
      S9       19  RD S5 (unique items)
? s s9 not (s6 or s7)
              19  S9
              28  S6
              22  S7
     S10      18  S9 NOT (S6 OR S7)
? t s10/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

 10/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12679520   21553151   PMID: 11696349
  Differential subcellular localization of hZip1 in adherent and
non-adherent cells.
  Milon B; Dhermy D; Pountney D; Bourgeois M; Beaumont C
  INSERM U409 and IFR Claude Bernard, Faculte Xavier Bichat, P.O. Box 416,
16 Rue Henri Huchard, 75018 Cedex 18, Paris, France.
  FEBS letters (Netherlands) Nov 2 2001, 507 (3) p241-6, ISSN
0014-5793 Journal Code: 0155157
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Two human divalent cation transporters of the ZIP family, hZip1 and
hZip2, homologous to Irt1 (Arabidopsis thaliana), the first
identified member, have been described. They were shown by transfection
into K562 cells to be localized at the plasma membrane and to mediate zinc
uptake. Here we report a differential subcellular localization of hZip1
according to cell type. By transient expressions of EGFP-hZip1, FLAG-tagged
or native hZip1, we observed that hZip1 has a vesicular localization in
COS-7 cells or in several epithelial cell lines, corresponding partially to
the endoplasmic reticulum. Using anti-hZip1 antibodies, we confirmed the
intracellular localization of the endogenous protein in PC-3, a prostate
cancer cell line.


 10/3,AB/2     (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11259916   21287186   PMID: 11389759
  Arabidopsis IRT2 gene encodes a root-periphery iron transporter.
  Vert G; Briat J F; Curie C
  Laboratoire de Biochimie et Physiologie Moleculaire des Plantes, UMR 5004
CNRS/INRA/Agro-M/Universite Montpellier II, 2 place Viala, F 34060
Montpellier CEDEX 1, France.
  Plant journal : for cell and molecular biology (England) Apr 2001, 26
(2) p181-9, ISSN 0960-7412 Journal Code: 9207397
```

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Iron uptake from the soil is a tightly controlled process in plant roots, involving specialized transporters. One such transporter, IRT1, was identified in **Arabidopsis** thaliana and shown to function as a broad-range metal ion transporter in yeast. Here we report the cloning and characterization of the IRT2 cDNA, a member of the ZIP family of metal transporters, highly similar to IRT1 at the amino-acid level. IRT2 expression in yeast suppresses the growth defect of iron and zinc transport yeast mutants and enhances iron uptake and accumulation. However, unlike IRT1, IRT2 does not transport manganese or cadmium in yeast. IRT2 expression is detected only in roots of A. thaliana plants, and is upregulated by iron deficiency. By fusing the IRT2 promoter to the uidA reporter gene, we show that the IRT2 promoter is mainly active in the external cell layers of the root subapical zone, and therefore provide the first tissue localization of a plant metal transporter. Altogether, these data support a role for the IRT2 transporter in iron and zinc uptake from the soil in response to iron-limited conditions.

10/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11227837 21249805 PMID: 11352462

Two iron-regulated cation transporters from tomato complement metal uptake-deficient yeast mutants.

Eckhardt U; Mas Marques A; Buckhout T J

Humboldt-Universitat zu Berlin, Institut fur Biologie, Angewandte Botanik, Germany. ulrich.eckhardt@rz.hu-berlin.de

Plant molecular biology (Netherlands) Mar 2001, 45 (4) p437-48, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Although iron deficiency poses severe nutritional problems to crop plants, to date iron transporters have only been characterized from the model plant **Arabidopsis** thaliana. To extend our molecular knowledge of Fe transport in crop plants, we have isolated two cDNAs (LeIRT1 and LeIRT2) from a library constructed from roots of iron-deficient tomato (Lycopersicon esculentum) plants, using the **Arabidopsis** iron transporter cDNA, IRT1, as a probe. Their deduced polypeptides display 64% and 62% identical amino acid residues to the IRT1 protein, respectively. Transcript level analyses revealed that both genes were predominantly expressed in roots. Transcription of LeIRT2 was unaffected by the iron status of the plant, while expression of LeIRT1 was strongly enhanced by iron limitation. The growth defect of an iron uptake-deficient yeast (Saccharomyces cerevisiae) mutant was complemented by LeIRT1 and LeIRT2 when ligated to a yeast expression plasmid. Transport assays revealed that iron uptake was restored in the transformed yeast cells. This uptake was temperature-dependent and saturable, and Fe2+ rather than Fe3+ was the preferred substrate. A number of divalent metal ions inhibited Fe2+ uptake when supplied at 100-fold or 10-fold excess. Manganese, zinc and copper uptake-deficient yeast mutants were also rescued by the two tomato cDNAs, suggesting that their gene products have a broad substrate range. The gene structure was determined by polymerase chain reaction experiments and, surprisingly, both genes are arranged in tandem with a tail-to-tail orientation.

10/3,AB/4 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA

3624570 20605899 Holding Library: ABL

Opioid peptide gene expression in the primary hereditary cardiomyopathy of the Syrian hamster. III. Autocrine stimulation of prodynorphin gene expression by dynorphin B

Ventura, C. Pintus, G.
University of Sassari, Sassari, Italy.

Bethesda, Md. : American Society for Biochemistry and Molecular Biology.
The Journal of biological chemistry. Mar 7, 1997. v. 272 (10) p. 6799-6804.
ISSN: 0021-9258 CODEN: JBCHA3
DNAL CALL NO: 381 J824
Language: English

Prodynorphin mRNA and dynorphin B expression have been previously shown to be greatly increased in cardiac myocytes of BIO 14.6 cardiomyopathic hamsters. Here we report that exogenous dynorphin B induced a dose-dependent increase in prodynorphin mRNA levels and stimulated prodynorphin gene transcription in normal hamster myocytes. Similar responses were elicited by the synthetic selective opioid receptor agonist U-50,488H. These effects were counteracted by the kappa opioid receptor antagonist Mr-1452 and were not observed in the presence of chelerythrine or calphostin C, two specific protein **kinase** C (PKC) inhibitors. Treatment of cardiomyopathic cells with Mr-1452 significantly decreased both prodynorphin mRNA levels and prodynorphin gene transcription. In control myocytes, dynorphin B induced the translocation of PKC-alpha to the nucleus and increased nuclear PKC activity without affecting the expression of PKC-delta,epsilon, or -**zeta**. Acute release of either U-50,488H or dyn B over single normal or cardiomyopathic cells transiently increased the cytosolic Ca2+ concentration. A sustained treatment with each opioid agonist increased the cytosolic Ca2+ level for a more prolonged period in cardiomyopathic than in control myocytes and led to a depletion of Ca2+ from the sarcoplasmic reticulum in both groups of cells. The possibility that prodynorphin gene expression may affect the function of the cardiomyopathic cell through an autocrine mechanism is discussed.

10/3,AB/6 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

10584196 Genuine Article#: 544DD Number of References: 42
Title: The **Arabidopsis** phospholipase D family. Characterization of a calcium-independent and phosphatidylcholine-selective PLD **zeta** 1 with distinct regulatory domains (ABSTRACT AVAILABLE)
Author(s): Qin CB; Wang XM (REPRINT)
Corporate Source: Kansas State Univ,Dept Biochem,Manhattan//KS/66506 (REPRINT); Kansas State Univ,Dept Biochem,Manhattan//KS/66506
Journal: PLANT PHYSIOLOGY, 2002, V128, N3 (MAR), P1057-1068
ISSN: 0032-0889 Publication date: 20020300
Publisher: AMER SOC PLANT BIOLOGISTS, 15501 MONONA DRIVE, ROCKVILLE, MD 20855 USA
Language: English Document Type: ARTICLE
Abstract: Four types of phospholipase D (PLD), PLDalpha, beta, gamma, and delta, have been characterized in **Arabidopsis**, and they display different requirements for Ca2+, phosphatidylinositol 4,5-bisphosphate (PIP,), substrate vesicle composition, and/or free fatty acids. However, all previously cloned plant PLDs contain a Ca2+-dependent phospholipid-binding C2 domain and require Ca2+ for activity. This study documents a new type of PLD, PLDzeta1, which is distinctively different from previously characterized PLDs. It contains at the N terminus a Phox homology domain and a pleckstrin homology domain, but not the C2 domain. A full-length cDNA for **Arabidopsis** PLDzeta1 has been identified and used to express catalytically active PLD in

Escherichia coli. PLDzeta1 does not require Ca2+ or any other divalent cation for activity. In addition, it selectively hydrolyzes phosphatidylcholine, whereas the other **Arabidopsis** PLDs use several phospholipids as substrates. PLDzeta1 requires PIP2 for activity, but unlike the PIP2-requiring PLDbeta or gamma, phosphatidylethanolamine is not needed in substrate vesicles. These differences are described, together with a genomic analysis of 12 putative **Arabidopsis** PLD genes that are grouped into alpha, beta, delta, gamma, and **zeta** based on their gene architectures, sequence similarities, domain structures, and biochemical properties.

10/3,AB/6 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07958476 Genuine Article#: 229KH Number of References: 40
Title: Nuclear localization of protein **kinase** C-alpha is regulated by 14-3-3 (ABSTRACT AVAILABLE)
Author(s): Zhang SS; Xing HM; Muslin AJ (REPRINT)
Corporate Source: WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT MED, BOX 8086, 660 S EUCLID AVE/ST LOUIS//MO/63110 (REPRINT); WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT MED/ST LOUIS//MO/63110; WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT CELL BIOL & PHYSIOL/ST LOUIS//MO/63110
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1999, V274, N35 (AUG 27), P 24865-24872
ISSN: 0021-9258 Publication date: 19990827
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: 14-3-3 proteins are intracellular, dimeric molecules that bind to and modify the activity of several signaling proteins. We used human 14-3-3 **zeta** as a bait in the yeast two-hybrid system to screen a murine embryonic cDNA library. One interacting clone was found to encode the carboxyl terminus of a putative protein **kinase**. The coding sequence of the human form (protein **kinase** C alpha, PKC alpha) of this protein **kinase** was found in GenBank(TM) on the basis of sequence homology. The two-hybrid clone was also highly homologous to TOUSLED, an **Arabidopsis** thaliana protein **kinase** that is required for normal flower and leaf development. PKC alpha has been found by coimmunoprecipitation to bind to 14-3-3 **zeta** in vivo. Our confocal laser immunofluorescence microscopic experiments revealed that PKC alpha colocalizes with the cytoplasmic intermediate filament system of cultured fibroblasts in the G(1) phase of the cell cycle. PKC alpha is found in the perinuclear area of S phase cells and in the nucleus of late G(2) cells. Transfection of cells with a dominant negative form of 14-3-3 eta promotes the nuclear localization of PKC alpha. These results suggest that the subcellular localization of PKC alpha is regulated, at least in part, by its association with 14-3-3.

10/3,AB/7 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07814896 Genuine Article#: 211NY Number of References: 58
Title: Plant MAP **kinase kinase kinases** structure, classification and evolution (ABSTRACT AVAILABLE)
Author(s): Jouannic S; Hamal A; Leprince AS; Tregear JW; Kreis M; Henry Y (REPRINT)
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, LAB BIOL DEV PLANTES, UMR 6818, BATIMENT 630 F-91405 ORSAY (FRANCE) (REPRINT ; UNIV

PARIS 11,INST BIOTECHNOL PLANTES, LAB BIOL DEV PLANTES, UMR 6818/F-91405 ORSAY//FRANCE/
Journal: GENE, 1999, V233, N1-2 (JUN 11), P1-11
ISSN: 0378-1119 Publication date: 19990611
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
Language: English Document Type: REVIEW
Abstract: The increasing number of reports describing plant MAP **kinase** signalling components reflects the cardinal role that MAP **kinase** pathways are likely to play during plant growth and development. Relationship and structural analyses of plant MAP **kinase kinase kinase** related cDNAs and genes established, on one hand, the PMEKKs, which may be distinguished into the alpha, beta, gamma, and **zeta** groups, and, on the other hand, the PRAFs that consist of the delta, eta and theta groups. Plant MAP3Ks are characterized by different primary structures, but conserved within a single group. A relationship analysis, which included animal, fungal and plant MAP3Ks, revealed a high degree of diversity among this biochemically established set of proteins, thus suggesting a range of biological functions. Four major families emerged, namely the MEKK/STE11, including the PMEKKs, the RAF, including the PRAFs, as well as the MLK and CDC7 families. These four families showed phylum-dependent distributions. Signature sequences characterizing the RAF family and the RAF subfamilies have been evidenced. However, no equivalent sequence motifs were identified for the MEKK/STE11 family, which is highly heterogeneous.

10/3,AB/8 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

07489949 Genuine Article#: 172TE Number of References: 53
Title: Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein **kinase** (ASK) multigene family (ABSTRACT AVAILABLE)
Author(s): Dornelas MC; Wittich P; vonRecklinghausen I; vanLammeren A; Kreis M (REPRINT)
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, ERS CNRS 569, BATIMENT 630/F-91405 ORSAY//FRANCE/ (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, ERS CNRS 569/F-91405 ORSAY//FRANCE/; AGR UNIV WAGENINGEN,LAB PLANT CYTOL & MORPHOL/NL-6703 BD WAGENINGEN//NETHERLANDS/
Journal: PLANT MOLECULAR BIOLOGY, 1999, V39, N1 (JAN), P137-147
ISSN: 0167-4412 Publication date: 19990100
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein **kinase** (ASK) multigene family, named ASKdzeta (ASK **zeta**), ASKetha (ASK eta) and ASKiota (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase **kinase**-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein **kinases** demonstrated a clear distinction

between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these **kinases**. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASK **zeta** is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.

10/3,AB/9 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06268890 Genuine Article#: YE942 Number of References: 24
Title: Subunit composition of pre-T cell receptor complexes expressed by primary thymocytes: CD3 delta is physically associated but not functionally required (ABSTRACT AVAILABLE)
Author(s): Berger MA (REPRINT) ; Dave V; Rhodes MF; Bosma GC; Bosma MJ; Kappes DJ; Wiest DL
Corporate Source: FOX CHASE CANC CTR,DIV BASIC SCI, IMMUNOBIOL WORKING GRP, 7701 BURHOLME AVE/PHILADELPHIA//PA/19111 (REPRINT)
Journal: JOURNAL OF EXPERIMENTAL MEDICINE, 1997, V186, N9 (NOV 3), P 1461-1467
ISSN: 0022-1007 Publication date: 19971103
Publisher: ROCKEFELLER UNIV PRESS, 1114 FIRST AVE, 4TH FL, NEW YORK, NY 10021
Language: English Document Type: ARTICLE
Abstract: Maturation of immature CD4(-)CD8(-)(DN) thymocytes to the CD4(+)CD8(+) (DP) stage of development is driven by signals transduced through a pre-T cell receptor (TCR) complex, whose hallmark is a novel subunit termed pre-T alpha (pT alpha). However, the precise role of pre-TCRs in mediating the DN to DP transition remains unclear. Moreover, progress In understanding pre-TCR function has been hampered thus far because previous attempts to demonstrate expression of pT alpha-containing pre-TCRs on the surface of normal thymocytes have been unsuccessful In this report, we demonstrate for the first time that pT alpha-containing pre-TCR complexes are expressed at low levels on the surface of primary thymocytes and that these pre-TCR complexes comprise a disulfide-linked pT alpha-TCR-beta heterodimer associated not only with CD3-gamma and -epsilon, as previously reported, but also with **zeta** and delta. Interestingly, while CD3-delta is associated with the pre-TCR complex, it is not required for pre-TCR function, evidenced by the generation of normal numbers of DP thymocytes in CD3-delta-deficient mice. The fact that any of the signaling components of the pre-TCR are dispensable for pre-TCR function is indeed surprising, given that few pre-TCR complexes are actually expressed on the surface of primary thymocytes in vivo. Thus, pre-TCRs do not require the full array of TCR-associated signaling subunits (gamma, delta, epsilon, and **zeta**), possibly because pT alpha itself possesses signaling capabilities.

10/3,AB/10 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06205693 Genuine Article#: YE663 Number of References: 43
Title: 14-3-3 inhibits the Dictyostelium myosin II heavy-chain-specific protein **kinase** C activity by a direct interaction: Identification of the 14-3-3 binding domain (ABSTRACT AVAILABLE)
Author(s): MattoYelin M; Aitken A; Ravid S (REPRINT)

Corporate Source: HEBREW UNIV JERUSALEM,HADASSAH MED SCH, DEPT BIOCHEM/IL-91120 JERUSALEM//ISRAEL/ (REPRINT); HEBREW UNIV JERUSALEM,HADASSAH MED SCH, DEPT BIOCHEM/IL-91120 JERUSALEM//ISRAEL/; NATL INST MED RES,LAB PROT STRUCT/LONDON NW7 1AA//ENGLAND/
Journal: MOLECULAR BIOLOGY OF THE CELL, 1997, V8, N10 (OCT), P1889-1899
ISSN: 1059-1524 Publication date: 19971000
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: Myosin II heavy chain (MHC) specific protein **kinase** C (MHC-PKC), isolated from Dictyostelium discoideum, regulates myosin II assembly and localization in response to the chemoattractant cyclic AMP. Immunoprecipitation of MHC-PKC revealed that it resides as a complex with several proteins. We show herein that one of these proteins is a homologue of the 14-3-3 protein (Dd14-3-3). This protein has recently been implicated in the regulation of intracellular signaling pathways via its interaction with several signaling proteins, such as PKC and Raf-1 **kinase**. We demonstrate that the mammalian 14-3-3 **zeta** isoform inhibits the MHC-PKC activity in vitro and that this inhibition is carried out by a direct interaction between the two proteins. Furthermore, we found that the cytosolic MHC-PKC, which is inactive, formed a complex with Dd14-3-3 in the cytosol in a cyclic AMP-dependent manner, whereas the membrane-bound active MHC-PKC was not found in a complex with Dd14-3-3. This suggests that Dd14-3-3 inhibits the MHC-PKC in vivo. We further show that MHC-PKC binds Dd14-3-3 as well as 14-3-3 **zeta** through its C1 domain, and the interaction between these two proteins does not involve a peptide containing phosphoserine as was found for Raf-1 **kinase**. Our experiments thus show an in vivo function for a member of the 14-3-3 family and demonstrate that MHC-PKC interacts directly with Dd14-3-3 and 14-3-3 **zeta** through its C1 domain both in vitro and in vivo, resulting in the inhibition of the **kinase**.

10/3,AB/11 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05955525 Genuine Article#: XK147 Number of References: 65
Title: An amphibian CD3 homologue of the mammalian CD3 gamma and delta genes (ABSTRACT AVAILABLE)
Author(s): Dzialo RC; Cooper MD (REPRINT)
Corporate Source: UNIV ALABAMA,WALLACE INST 378, DEPT MED, DIV DEV & CLIN IMMUNOL/BIRMINGHAM/AL/35294 (REPRINT); UNIV ALABAMA,WALLACE INST 378, DEPT MED, DIV DEV & CLIN IMMUNOL/BIRMINGHAM/AL/35294; UNIV ALABAMA,DEPT PEDIAT, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294; UNIV ALABAMA,DEPT MICROBIOL, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294; HOWARD HUGHES MED INST,/BIRMINGHAM/AL 35294
Journal: EUROPEAN JOURNAL OF IMMUNOLOGY, 1997, V27, N7 (JUL), P1640-1647
ISSN: 0014-2980 Publication date: 19970700
Publisher: VCH PUBLISHERS INC, 303 NW 12TH AVE, DEERFIELD BEACH, FL 33442-1788
Language: English Document Type: ARTICLE
Abstract: T cell receptor (TCR) genes have been identified in representatives of both cartilaginous and bony vertebrates. The CD3 chains that serve as signal transducing elements of the TCR complex in mammals have been defined to a limited extent in birds. In these studies a CD3 homologue was identified in an amphibian representative, Xenopus laevis, using degenerate oligomer primers designed from conserved regions of avian and mammalian CD3 gamma/delta subunits. The reverse transcriptase polymerase chain reaction amplified product of Xenopus splenocyte RNA was then used to isolate full-length cDNA clones from a splenic library. When employed as probes, the cDNA clones hybridized with a 1-kb mRNA transcript in Xenopus T cells, but not in

other cell types. Comparison of the deduced amino acid sequence indicated a similar degree of homology with mammalian and avian CD3 gamma and delta chains. Genomic analysis indicated that the Xenopus CD3 molecule is encoded by five exons, a structure resembling the mammalian CD3 delta gene rather than the seven exon CD3 gamma gene. Southern blot analysis and sequencing of the 5' flanking region failed to yield evidence of a related Xenopus gene. This amphibian CD3 gene thus appears to represent an ancestral form of the mammalian CD3 gamma and delta genes.

10/3,AB/12 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05916662 Genuine Article#: XG579 Number of References: 45
Title: A spontaneously arising mutation in the DLAARN motif of murine ZAP-70 abrogates **kinase** activity and arrests thymocyte development (ABSTRACT AVAILABLE)
Author(s): Wiest DL; Ashe JM; Howcroft TK; Lee HM; Kemper DM; Negishi I; Singer DS; Singer A (REPRINT) ; Abe R
Corporate Source: FOX CHASE CANC CTR,DIV BASIC SCI/PHILADELPHIA//PA/19111 (REPRINT); NCI,EXPT IMMUNOL BRANCH, NIH/BETHESDA//MD/20892; USN,MED RES INST, IMMUNE CELL BIOL DEPT/BETHESDA//MD/20889; NIPPON ROCHE RES CTR,/KAMAKURA/KANAGAWA 247/JAPAN/; SCI UNIV TOKYO,RES INST BIOL SCI, DIV IMMUNOBIOL/TOKYO/CHIBA 278/JAPAN/
Journal: IMMUNITY, 1997, V6, N6 (JUN), P663-671
ISSN: 1074-7613 Publication date: 19970600
Publisher: CELL PRESS, 1050 MASSACHUSETTES AVE, CIRCULATION DEPT, CAMBRIDGE, MA 02138
Language: English Document Type: ARTICLE
Abstract: Development of immature CD4(+)CD8(+) thymocytes into functionally mature CD4(+) and CD8(+) T cells is driven by selection events that require signals transduced through the T cell antigen receptor (TCR). Transduction of TCR signals in the thymus involves tyrosine phosphorylation of the protein tyrosine **kinase** ZAP-70 by p56(lck) and results in induction of ZAP-70 enzymatic activity. We have identified a novel, spontaneously arising point mutation within a highly conserved motif (DLAARN) in the **kinase** domain of murine ZAP-70 that uncouples tyrosine phosphorylation of ZAP-70 from induction of ZAP-70 **kinase** activity. Mice homozygous for this mutation are devoid of mature T cells because thymocyte development is arrested at the CD4(+)CD8(+) stage of differentiation. The developmental arrest is due to the inability of CD4(+)CD8(+) thymocytes to propagate TCR signals in the absence of ZAP-70 **kinase** activity despite tyrosine phosphorylation of TCR-associated ZAP-70 molecules.

10/3,AB/13 (Item 9 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05883644 Genuine Article#: XE034 Number of References: 54
Title: Subcellular localization and ubiquitin-conjugating enzyme (E2) interactions of mammalian HECT family ubiquitin protein ligases (ABSTRACT AVAILABLE)
Author(s): Hatakeyama S; Jensen JP; Weissman AM (REPRINT)
Corporate Source: NCI,LAB IMMUNE CELL BIOL, DIV BASIC SCI, NIH, BLDG 10, RM 1B34, 9000 ROCKVILLE /BETHESDA//MD/20892 (REPRINT); NCI,LAB IMMUNE CELL BIOL, DIV BASIC SCI, NIH/BETHESDA//MD/20892
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N24 (JUN 13), P 15085-15092
ISSN: 0021-9258 Publication date: 19970613
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE

PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: In most instances, the transfer of ubiquitin to target proteins is catalyzed by the action of ubiquitin protein ligases (E3s). Full-length cDNAs encoding murine E6-associated protein (mE6-AP) as well as Nedd-4, a protein that is homologous to E6-AP in its C terminus, were cloned. Nedd-4 and mouse E6-AP are both enzymatically active E3s and function with members of the UbcH5 family of E2s. Mouse E6-AP, like its human counterpart, ubiquitinates p53 in the presence of human papilloma virus E6 protein, while Nedd-4 does not. Consistent with its role in p53 ubiquitination, mE6-AP was found both in the nucleus and cytosol, while Nedd-4 was found only in the cytosol. Binding studies implicate a 150-amino acid region that is 40% identical between mE6-AP and Nedd-4 as a binding site for the C terminal portion of an E2 enzyme (UbcH5B). Nedd-4 was determined to have a second nonoverlapping E2 binding site that recognizes the first 67 amino acids of UbcH5B but not the more C-terminal portion of this E2. These findings provide the first demonstration of physical interactions between mammalian E2s and E3s and establish that these interactions occur independently of ubiquitin and an intact E3 catalytic domain. Furthermore, the presence of two E2 binding sites within Nedd-4 suggests models for ubiquitination involving multiple E2 enzymes associated with E3s.

10/3,AB/14 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05821731 Genuine Article#: XA029 Number of References: 60
Title: 14-3-3 epsilon positively regulates Ras-mediated signaling in Drosophila ABSTRACT AVAILABLE)
Author(s): Chang HC; Rubin GM (REPRINT)
Corporate Source: UNIV CALIF BERKELEY,HOWARD HUGHES MED INST, DEPT CELL & MOL BIOL/BERKELEY//CA/94720 (REPRINT); UNIV CALIF BERKELEY,HOWARD HUGHES MED INST, DEPT CELL & MOL BIOL/BERKELEY//CA/94720
Journal: GENES & DEVELOPMENT, 1997, V11, N9 (MAY 1), P1132-1139
ISSN: 0890-9369 Publication date: 19970501
Publisher: COLD SPRING HARBOR LAB PRESS, 1 BUNGTOWN RD, PLAINVIEW, NY 11724
Language: English Document Type: ARTICLE
Abstract: We have isolated mutations in the gene encoding a Drosophila 14-3-3 epsilon protein as suppressors of the rough eye phenotype caused by the ectopic expression of RAS1(V12). Using a simple loss-of function 14-3-3 epsilon mutation, we show that 14-3-3 epsilon acts to increase the efficiency of RAS1 signaling. The 14-3-3 epsilon protein appears to function in multiple RTK pathways, suggesting that it is a general component of RAS1 signaling cascade. Sequence analysis of three dominant-negative alleles defines two regions of 14-3-3 epsilon that participate in RAS1 signaling. We also present evidence that 14-3-3 epsilon and 14-3-3 **zeta**, two 14-3-3 protein family members, are partially redundant for RAS1 signaling in photoreceptor formation and in animal viability. Our genetic data suggest that 14-3-3 epsilon functions downstream of or parallel to RAF, but upstream of nuclear factors in RAS1 signaling.

10/3,AB/15 (Item 11 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05757886 Genuine Article#: WV968 Number of References: 71
Title: The interchain disulfide bond between TCR alpha beta heterodimers on human T cells is not required for TCR CD3 membrane expression and signal transduction (ABSTRACT AVAILABLE)

Author(s): Arnaud J; Hucheng A; Vernhes MC; CasparBauguil S; Lenfant F; Sancho J; Terhorst C; Rubin B (REPRINT)
Corporate Source: CHU PURPAN,CELLULAR & MOL IMMUNOL LAB, CTR IMMUNOPATHOL & GENET HUMAINE, CIGH, CNRS/F-31300 TOULOUSE//FRANCE/ (REPRINT); CHU PURPAN,CELLULAR & MOL IMMUNOL LAB, CTR IMMUNOPATHOL & GENET HUMAINE, CIGH, CNRS/F-31300 TOULOUSE/ FRANCE'; CHU PURPAN,INSERM, U395/F-31300 TOULOUSE/ /FRANCE ; CSIC,DEPT BIOL CELULAR & INMUNOL/GRANADA 18001//SPAIN/; HARVARD UNIV,SCH MED, BETH ISRAEL HOSP, DIV IMMUNOL/BOSTON//MA/02215
Journal: INTERNATIONAL IMMUNOLOGY, 1997, V9, N4 (APR), P615-626
ISSN: 0953-8178 Publication date: 19970400
Publisher: OXFORD UNIV PRESS, WALTON ST JOURNALS DEPT, OXFORD, ENGLAND OX2 6DP
Language: English Document Type: ARTICLE
Abstract: In the present paper, it was attempted to define the amino acids or regions on TCR beta molecules that determine the TCR alpha-TCR beta interaction. Sequence studies on HBP-ALL variant cells with an intrinsic deficiency in TCR alpha beta dimer formation elucidated a conserved amino acid motif in the TCR-C-beta beta-strand E, = Y(C)(L)(S)SRLR(V)(S)(A); this motif seems to represent one interaction area for the TCR alpha-TCR beta interaction. In addition, amino acids in the connecting peptide may be shaped in a precise structure (by the interactions with CD3 molecules?) involved in TCR alpha-TCR beta dimerization. This result was supported by the finding that the interchain disulfide bond between TCR alpha and beta chains is not required for membrane expression or transmembrane signal transduction of TCR alpha beta-CD3 complexes. Finally, comparative results from two membrane TCR-CD3-negative Jurkat variants R4.9 and E6.E12 suggest that TCR-C-beta exon 1- and 2-encoded amino acids are important for the TCR beta/CD3 gamma epsilon association.

10/3,AB/16 (Item 12 from file: 34)
DIALOG(R File 34:SciSearch(R Cited Ref Sci
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08754761 Genuine Article#: WV741 Number of References: 57
Title: Role of CD3 gamma and CD3 delta cytoplasmic domains in cytolytic T lymphocyte functions and TCR/CD3 down-modulation (ABSTRACT AVAILABLE)
Author(s): Luton F; Buferne M; Legendre V; Chauvet E; Boyer C; Schmitt-Verhulst AM (REPRINT)
Corporate Source: CTR IMMUNOL,INSERM, CNRS MARSEILLE LUMINY, PARC SCI LUMINY, CASE 906 F-13288 MARSEILLE 9//FRANCE/ (REPRINT); CTR IMMUNOL,INSERM, CNRS MARSEILLE LUMINY/F-13288 MARSEILLE 9//FRANCE/
Journal: JOURNAL OF IMMUNOLOGY, 1997, V158, N9 (MAY 1), P4162-4170
ISSN: 0022-1767 Publication date: 19970501
Publisher: AMER ASSOC IMMUNOLOGISTS, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: TCR engagement leads to down-modulation of TCR/CD3 complexes from the T cell surface. The importance of this effect in T cell physiology is unknown. Here, we characterized a CTL clone deficient in TCR/CD3 surface expression that had lost both CD3 delta and CD3 gamma mRNA, allowing us to address the role of these chains in the assembly, signaling, and dynamics of the TCR/CD3 complex. Expression of either CD3 delta or CD3 gamma alone failed to reconstitute surface expression of the TCR/CD3 complex, but reconstitution with a cytoplasmically truncated CD3 delta (delta t) and a native (gamma) or cytoplasmically truncated (gamma t) human CD3 gamma led to reexpression of TCR/CD3 complexes in both cases. This indicated that CD3 delta and CD3 gamma assume specific functions in TCR/CD3 assembly independently of their cytoplasmic domains. The delta t gamma t variant specifically killed target cells, expressed the IFN-gamma gene in response to Ag, and produced TNF-alpha in response to anti-CD3 mAb, but it was affected in

CD3 ligand-induced TCR/CD3 down-modulation. Both PMA- and CD3 ligand-induced TCR/CD3 down-modulation were defective in the delta t gamma t variant, whereas the delta t gamma variants were unaffected, and previously described delta gamma t variants were affected only in PMA-induced down-modulation, Specific protein **kinase** C (PKC) inhibitors indicated that PMA- but not CD3 ligand-induced down-modulation was dependent on PKC activity. Thus, amino acid sequences present in either the CD3 delta or CD3 gamma cytoplasmic domain control ligand-induced TCR/CD3 down-modulation, and neither these sequences nor this property are required for cytolysis and IFN-gamma gene expression in response to Ag.

10/3,AB/17 (Item 13 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05533314 Genuine Article#: WE924 Number of References: 8
Title: Purification of the T-cell receptor **zeta**-chain: Covalent modification by 4-(2-aminoethyl)benzenesulfonyl fluoride
Author(s): Sweeney B (REPRINT) ; Proudfoot K; Parton AH; King LM; Slocombe P; Perry MJ
Corporate Source: CELLTECH LTD,216 BATH RD/SLOUGH SL1 4EN/BERKS/ENGLAND/ (REPRINT)
Journal: ANALYTICAL BIOCHEMISTRY, 1997, V245, N1 (FEB 1), P107-109
ISSN: 0003-2697 Publication date: 19970201
Publisher: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495
Language: English Document Type: ARTICLE

10/3,AB/18 (Item 14 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05515605 Genuine Article#: WD587 Number of References: 25
Title: Protein expression of the epsilon subspecies of protein **kinase** C ceases asSwiss 3T6 fibroblasts increase in cell density even though message for theprotein is still present (ABSTRACT AVAILABLE)
Author(s): Littlebury P; Watson J; Williams T; Beale G; Rumsby M (REPRINT)

Corporate Source: UNIV YORK,DEPT BIOL/YORK YO1 5YW/N YORKSHIRE/ENGLAND/ (REPRINT); UNIV YORK,DEPT BIOL/YORK YO1 5YW/N YORKSHIRE/ENGLAND/
Journal: FEBS LETTERS, 1997, V400, N3 (JAN 6), P304-308
ISSN: 0014-5793 Publication date: 19970106
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: We have noted previously that growth of C6 glioma cells from low cell density to confluency and quiescence in serum in accompanied by changes in protein content of different protein **kinase** C (PKC) subspecies. Here we show that the same occurs as non-contact-inhibiting Swiss 3T6 fibroblasts grow to high density in the presence of serum. Protein expression of PKC subspeciesalpha and delta increases as the cells increase in density while that of PKC-**zeta** remains the same. Unusually, protein expression of PKC-epsilon is completely down-regulated as cells grow beyond about 50% confluency and no PKC-epsilon protein can be detected in 3T6 fibroblasts at high density by Western blotting. However, mRNA for PKC-epsilon is expressed at all stages offibroblast growth as revealed by RT-PCR. When high-density 3T6 fibroblastsare passaged to low density in fresh medium, re-expression of PKC-epsilon protein is observed within 15 min and becomes down-regulated as cells become more dense. This very rapid synthesis of PKC-epsilon is not blocked by the transcription inhibitor actinomycin D but is inhibited by cycloheximide. PKC-epsilon has some characteristics

of a novel 'early response' protein whose synthesis in newly passaged 3T6 cells is regulated at the translationallevel.

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Set      Items   Description
S1        7347   ARABIDOPSIS AND KINAS?
S2          90   S1 AND SHAGGY
S3          55   S1 AND ASK
S4           0   S1 AND DZETA
S5          21   S1 AND ZETA
S6          28   RD S2 (unique items)
S7          22   RD S3 (unique items)
S8          16   S7 NOT S6
S9          19   RD S5 (unique items)
S10         18   S9 NOT (S6 OR S7)
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           40199  ZETA
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           95824  ARABIDOPSIS
     S12       0  S11 AND ARABIDOPSIS
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 removal, customized scheduling. See HELP ALERT.
   File   5:Biosis Previews(R)  1969-2002/Jul W3
          (c) 2002 BIOSIS
 *File   5: Alert feature enhanced for multiple files, duplicates
 removal, customized scheduling. See HELP ALERT.
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 *File   6: Alert feature enhanced for multiple files, duplicates
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          (c) 2002 CAB International
 *File  50: Truncating CC codes is recommended for full retrieval.
 See Help News50 for details.
   File  65:Inside Conferences  1993-2002/Jul W4
          (c) 2002 BLDSC all rts. reserv.
   File  76:Life Sciences Collection  1982-2002/Jul
          (c) 2002 Cambridge Sci Abs
   File  94:JICST-EPlus  1985-2002/Jun W1
          (c)2002 Japan Science and Tech Corp(JST)
 *File  94: There is no data missing. UDs have been adjusted to reflect
  the current months data. See Help News94 for details.
   File  98:General Sci Abs/Full-Text  1984-2002/Jun
          (c) 2002 The HW Wilson Co.
   File  99:Wilson Appl. Sci & Tech Abs  1983-2002/Jun
          (c) 2002 The HW Wilson Co.
   File 117:Water Resour.Abs.  1967-2002/Jun
          (c) 2002 Cambridge Scientific Abs.
   File 143:Biol. & Agric. Index  1983-2002/Jun
          (c) 2002 The HW Wilson Co
   File 144:Pascal  1973-2002/Jul W4
          (c) 2002 INIST/CNRS
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         Dist by NAL, Intl Copr. All rights reserved
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          (c) 2002 PJB Publications,Ltd.
   File 266:FEDRIP  2002/Jun
         Comp & dist by NTIS, Intl Copyright All Rights Res
   File 306:Pesticide Fact File  1998/Jun
          (c) 1998 BCPC
 *File 306: File has been updated & reloaded.  See HELP NEWS 306.  New
 Bluesheet available in P415 & at URL http://library.dialog.com/bluesheets.
   File 357:Derwent Biotech Res.  1982-2002/June W1
          (c) 2002 Thomson Derwent & ISI
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*File 357: File enhancements now online. See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
  File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
        (c) 1998 Inst for Sci Info

      Set Items Description
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>>>Duplicate detection is not supported for File 306.

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 2/3,AB/1   (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10186524   99178801   PMID: 10080716
  Characterization of three novel members of the Arabidopsis SHAGGY-related protein kinase (ASK) multigene family.
  Lomelas M C; Wittich P; von Recklinghausen I; van Lammeren A; Kreis M
  Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris-Sud, Orsay, France.
  Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47,
ISSN 0167-4412 Journal Code: 9106343
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  In this paper we report the characterization of three novel members of the Arabidopsis shaggy-related protein kinase (ASK) multigene family, named **ASKdzeta** (ASKzeta), ASKetha (ASKeta) and ASKiota (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the Arabidopsis genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

 2/3,AB/2   (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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02359959 4495739

Characteriztion of three novel members of the Arabidopsis SHAGGY-related protein kinase (ASK) multigene family
Dornelas, M.C.; Wittich, P.; von Recklinghausen, I.; van Lammeren, A.; Kreis, M.
Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris Sud, Batiment 630, 91405 Orsay Cedex, France
Plant Molecular Biology vol. 39, no. 1, pp. 137-147 (1999)
ISSN: 0167-4412
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Genetics Abstracts; Biochemistry Abstracts 2: Nucleic Acids

In this paper we report the characterization of three novel members of the Arabidopsis shaggy-related protein kinase (ASK) multigene family, named **ASKdzeta** (ASK), ASKetha (ASK eta) and ASKiota (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the Arabidopsis genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASK\g?\ is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha , ASK gamma and ASK iota in developing embryos.

2/3,AB/2 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

14249199 PASCAL No.: 99-0452372
Caracterisation d'homologues de la proteine kinase SHAGGY chez Arabidopsis thaliana et leur role biologique pendant le developpement
(Characterization of Arabidopsis thaliana homologues of SHAGGY protein kinase and their biological role during development)
DORNELAS Marcelo; KREIS Martin, dir
Universite de Paris 11, Orsay, France
Univ., Universite de Paris 11, Orsay, FRA Degree: Th. doct.
1999-05; 1999 182 p.
Language: French Summary Language: French; English
Trois nouveaux membres de la famille multigenique ASK (pour Arabidopsis SHAGGY - related protein kinases) nommes **ASKdzeta** (ASK zeta), ASKetha (ASK eta) et ASKiota (ASK iota), ont ete identifies chez Arabidopsis thaliana. Les genes ASK sont des homologues vegetaux du gene SHAGGY (SGG) chez la Drosophila, appartenant a la sous-famille GSK-3 des proteines kinases. Dans un premier temps, la comparaison des sequences d'acides amines des proteines kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, evolutivement conserves, d'homologues vegetaux de SGG. La comparaison des sequences nucleotidiques des genes de la famille ASK a permis la proposition d'un modele d'evolution de cette famille multigenique. Par la suite, l'expression des genes ASK des groupes I et II a ete etudiee pendant le developpement d'Arabidopsis utilisant la technique d'hybridation in situ. Des plantes transgeniques contenant des constructions antisens des genes ASK des groupes I et II ont ete obtenues.

L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les proteines ASK pendant le developpement floral et embryonnaire d'Arabidopsis.

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              6  S1
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E3         1  *AU=DORNELAS MARCELO
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E10        2   AU=DORNELAS, E.A.
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           95824   ARABIDOPSIS
      S5      12   S4 AND ARABIDOPSIS
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>->Duplicate detection is not supported for File 306.

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? t s6/3,ab/all
>->No matching display code(s) found in file(s): 65, 235, 306

 6/3,AB/1      (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10692822   20223136   PMID: 10758494
  Arabidopsis thaliana SHAGGY-related protein kinases (AtSK11 and 12)
function in perianth and gynoecium development.
  Dornelas M C; Van Lammeren A A; Kreis M
  Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP),
UMR/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France
  Plant journal : for cell and molecular biology (ENGLAND)   Mar 2000,  21
 (5)  p419-29,  ISSN 0960-7412   Journal Code: 9207397
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  In higher plants, the correct patterning of the floral meristem in terms
of organ type, number and form is the result of a concerted expression of a
network of genes. We describe phenotypes of flower patterning, resulting
from a reduction of transcript levels of the Arabidopsis
SHAGGY-related protein kinase genes AtSK11(ASKalpha) and AtSK12(ASKgamma).
The AtSK genes are plant homologues of the Drosophila shaggy (SGG) gene and
the mammalian Glycogen-Synthase Kinase 3 (GSK-3). The SGG protein kinase is
a key component of the wingless signalling pathway and is required for the
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establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASKalpha and AtSK12(ASKgamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASKalpha) and AtSK12(ASKgamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASKalpha) and AtSK12(ASKgamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

6/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10135524 99178801 PMID: 10080716
Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein kinase (ASK) multigene family.
Dornelas M C; Wittich P; von Recklinghausen I; van Lammeren A; Kreis M
Institut de Biotechnologie des Plantes EPS/CNRS 569, Universite de Paris-Sud, Orsay, France.
Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47, ISSN 0167-4412 Journal Code: 9106343
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein kinase (ASK) multigene family, named ASKdzeta (ASKzeta), ASKetha (ASKeta) and ASKiota (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

6/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09842008 98278841 PMID: 9611268
The **Arabidopsis** SHAGGY-related protein kinase (ASK) gene family: structure, organization and evolution.
Dornelas M C; Lejeune B; Dron M; Kreis M
Institut de Biotechnologie des Plantes, EPS CNRS 569, Universite de

Paris-Sud, Batiment 630, F-91405, Orsay, Cedex, France.
Gene (NETHERLANDS) Jun 8 1998, 212 (2) p249-57, ISSN 0378-1119
Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein kinase domain about 70% identical to SHAGGY protein kinase (SGG) and glycogen synthase kinase-3 (GSK-3), respectively, from Drosophila and mammals. In this study we have characterized the structure and evolution of the **Arabidopsis** SHAGGY-related protein kinase (ASK) gene family. At least ten ASK genes are present per haploid genome of **Arabidopsis**. The genomic sequences of five ASK genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the **Arabidopsis** gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted ASK genes were mapped and shown to be dispersed over the five **Arabidopsis** chromosomes. A tentative model for the organization and evolution of the **Arabidopsis** ASK genes is presented.

6/3,AB/4 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

10695093 Genuine Article#: 557GG Number of References: 32
Title: A genomic approach to elucidating grass flower development (ABSTRACT AVAILABLE)
Author(s): **Dornelas MC (REPRINT)** ; Rodriguez APM
Corporate Source: USP,Escola Super Agr Luiz de Queiroz, Dept Ciencias Florestais,Av Padua Dias 11/BR-13418900 Piracicaba/SP/Brazil/ (REPRINT) ; USP,Escola Super Agr Luiz de Queiroz, Dept Ciencias Florestais,BR-13418900 Piracicaba/SP/Brazil/; USP,Ctr Energia Nucl Agr, Lab Biotecnol Vegetal,BR-13400970 Piracicaba/SP/Brazil/
Journal: GENETICS AND MOLECULAR BIOLOGY, 2001, V24, N1-4, P69-76
ISSN: 1415-4757 Publication date: 20010000
Publisher: SOC BRASIL GENETICA, RUA CAP ADELMIO NORBET DA SILVA, 736, ALTO DA BOA VISTA, 14025-670 RIBEIRAO PRET, BRAZIL
Language: English Document Type: ARTICLE
Abstract: In sugarcane (Saccharum sp) as with other species of grass, at a certain moment of its life cycle the vegetative meristem is converted into an inflorescence meristem which has at least two distinct inflorescence branching steps before the spikelet meristem terminates in the production of a flower (floret). In model dicotyledonous species such successive conversions of meristem identities and the concentric arrangement of floral organs in specific whorls have both been shown to be genetically controlled. Using data from the Sugarcane Expressed Sequence Tag (EST) Project (SUCEST) database, we have identified all sugarcane proteins and genes putatively involved in reproductive meristem and flower development. Sequence comparisons of known flower-related genes have uncovered conserved evolutionary pathways of flower development and flower pattern formation between dicotyledons and monocotyledons, such as some grass species. We have paid special attention to the analysis of the MADS-box multigene family of transcription factors that together with the APETALA2 (AP2) family are the key elements of the transcriptional networks controlling plant reproductive development. Considerations on the evolutionary developmental genetics of grass flowers and their relation to the ABC homeotic gene activity model of flower development are also presented.

6/3,AB/5 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

14249399 PASCAL No.: 99-0452372
Caracterisation d'homologues de la proteine kinase SHAGGY chez **Arabidopsis** thaliana et leur role biologique pendant le developpement
(Characterization of **Arabidopsis** thaliana homologues of SHAGGY protein kinase and their biological role during development)
DORNELAS Marcelo; KREIS Martin, dir
Universite de Paris 11, Orsay, Francee
Univ.: Universite de Paris 11, Orsay, FRA Degree: Th. doct.
1999-05; 1999 182 p.
Language: French Summary Language: French; English
Trois nouveaux membres de la famille multigenique ASK (pour **Arabidopsis** SHAGGY - related protein kinases) nommes ASKdzeta (ASK zeta), ASKetha (ASK eta) et ASKiota (ASK iota), ont ete identifies chez **Arabidopsis** thaliana. Les genes ASK sont des homologues vegetaux du gene SHAGGY (SGG) chez la Drosophila, appartenant a la sous-famille GSK-3 des proteines kinases. Dans un premier temps, la comparaison des sequences d'acides amines des proteines kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, evolutivement conserves, d'homologues vegetaux de SGG. La comparaison des sequences nucleotidiques des genes de la famille ASK a permis la proposition d'un modele d'evolution de cette famille multigenique. Par la suite, l'expression des genes ASK des groupes I et II a ete etudiee pendant le developpement d'**Arabidopsis** utilisant la technique d'hybridation in situ. Des plantes transgeniques contenant des constructions antisens des genes ASK des groupes I et II ont ete obtenues. L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les proteines ASK pendant le developpement floral et embryonnaire d'**Arabidopsis**.

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 11 3,AB/1      (Item 1 from file: 76)
DIALOG(R)File  76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02705721 5357176
Condensin and cohesin knockouts in Arabidopsis exhibit a titan seed
  phenotype
Liu, Chun ming; McElver, J.; Tzafrir, I.; Joosen, R.; Wittich, P.; Patton,
  D.; Van Lammeren, A.A.M.; Meinke, D.
Department of Botany, Oklahoma State University, Stillwater, OK 74078, USA
Plant Journal  vol. 29, no. 4, pp. 405-415  (2002)
ISSN: 0960-7412
DOCUMENT TYPE: Journal article  LANGUAGE: ENGLISH
SUBFILE: Genetics Abstracts

   The titan (ttn) mutants of Arabidopsis exhibit striking
alterations in chromosome dynamics and cell division during seed
development. Endosperm defects include aberrant mitoses and giant polyploid
nuclei. Mutant embryos differ in cell size, morphology and viability,
depending on the locus involved. Here we demonstrate that three TTN genes
encode chromosome scaffold proteins of the condensin (SMC2) and cohesin
(SMC1 and SMC3) classes. These proteins have been studied extensively in
yeast and animal systems, where they modulate chromosome condensation,
chromatid separation, and dosage compensation. Arabidopsis contains
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single copies of SMC1 and SMC3 cohesins. We used forward genetics to identify duplicate T-DNA insertions in each gene. These mutants (ttn7 and ttn8) have similar titan phenotypes: giant endosperm nuclei and arrested embryos with a few small cells. A single SMC2 knockout (ttn3) was identified and confirmed by molecular complementation. The weak embryo phenotype observed in this mutant may result from expression of a related gene (AtSMC2) with overlapping functions. Further analysis of titan mutants and the SMC gene family in **Arabidopsis** should provide clues to chromosome mechanics in plants and insights into the regulation of nuclear activity during endosperm development.

11/3,AB/2 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

02479619 4699031
Arabidopsis thaliana SHAGGY-related protein kinases (AtSK11 and 12) function in perianth and gynoecium development
Dornelas, M.C.; **van Lammeren, A.A.M.**; Kreis, M.
Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP), UMR/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France
Plant Journal vol. 21, no. 5, pp. 419-429 (2000)
ISSN: 0960-7412
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Genetics Abstracts

In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11(ASK alpha) and AtSK12(ASK gamma). The AtSK genes are plant homologues of the Drosophila shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASK alpha) and AtSK12(ASK gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASK alpha) and AtSK12(ASK gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASK alpha) and AtSK12(ASK gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.
?

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E9         7   AU=VANLAMMEREN FM
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E11        5   AU=VANLAMMEREN JPM
E12        1   AU=VANLAMMEREN R

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            95824  ARABIDOPSIS
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>>>No matching display code(s) found in file(s): 65, 235, 306

 15/3,AB/1      (Item 1 from file: 34)
DIALOG(R)File  34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

08660974   Genuine Article#: 313JP   Number of References: 31
Title: Structure and development of somatic embryos formed in
    Arabidopsis thaliana pt mutant callus cultures derived from
    seedlings  (ABSTRACT AVAILABLE)
Author(s): vonRecklinghausen IR; Iwanowska A; Kieft H; Mordhorst AP; Schel
    JHN; vanLammeren AAM  (REPRINT)
Corporate Source: WAGENINGEN UNIV AGR,LAB EXPT MORPHOL & CELL BIOL,
    ARBORETUMLAAN 4/NL-6703 BD WAGENINGEN//NETHERLANDS/ (REPRINT);
    WAGENINGEN UNIV AGR,LAB EXPT MORPHOL & CELL BIOL/NL-6703 BD
    WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,MOL BIOL LAB/NL-6703 BD
    WAGENINGEN//NETHERLANDS/
Journal: PROTOPLASMA, 2000, V211, N3-4, P217-224
ISSN: 0033-183X   Publication date: 20000000
Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201
    VIENNA, AUSTRIA
Language: English   Document Type: ARTICLE
Abstract: Seeds of the Arabidopsis thaliana mutant primordia timing
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(pt) were germinated in 2,4-dichlorophenoxyacetic acid-containing liquid medium. The seedlings formed somatic embryos and nonembryogenic and embryogenic callus in vitro in a time period of approximately two to three weeks. Embryogenesis and callus formation were monitored with respect to origin, structure, and development. Ten days after germination globular structures appeared in close vicinity of and on the shoot apical meristem (SAM). Somatic embryos formed either directly on the SAM region of the seedling or indirectly on embryogenic callus that developed at the SAM zone. Globular structures developed along the vascular tissue of the cotyledons as well, but only incidentally they formed embryos. Upon deterioration, the cotyledons formed callus. Regular subculture of the embryogenic callus gave rise to high numbers of somatic embryos. Such primary somatic embryos, grown on callus, originated from meristematic cell clusters located under the surface of the callus. Embryos at the globular and heart-shape stage were mostly hidden within the callus. Embryos at torpedo stage appeared at the surface of the callus because their axis elongated. Secondary somatic embryos frequently formed directly on primary ones. They preferentially emerged from the SAM region of the primary somatic embryos, from the edge of the cotyledons, and from the hypocotyl. We conclude that the strong regeneration capacity of the pt mutant is based on both recurrent and indirect embryogenesis.

15/3,AB/2 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

08560880 Genuine Article#: 300TZ Number of References: 51
Title: **Arabidopsis** thaliana SHAGGY-related protein kinases (AtSK11 and 12) function in perianth and gynoecium development (ABSTRACT AVAILABLE)
Author(s): Dornelas MC; **vanLammeren AAM**; Kreis M (REPRINT)
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618, BATIMENT 630/F-91405 ORSAY//FRANCE (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618,F-91405 ORSAY//FRANCE/; AGR UNIV WAGENINGEN,LAB EXPT PLANT MORPHOL & CELL BIOL/NL 6703 BD WAGENINGEN//NETHERLANDS/
Journal: PLANT JOURNAL, 2000, V21, N5 MAR, P419-429
ISSN: 0960-7412 Publication date: 20000300
Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND
Language: English Document Type: ARTICLE
Abstract: In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11(ASK alpha) and AtSK12(ASK gamma). The AtSK genes are plant homologues of the Drosophila shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASK alpha) and AtSK12-ASK gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASK alpha) and AtSK12(ASK gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASK alpha) and AtSK12(ASK gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the

apical-basal patterning of the gynoecium.

15/3,AB/3 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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08315411 Genuine Article#: 270KW Number of References: 37
Title: beta-tubulin accumulation and DNA synthesis are sequentially resumed in embryo organs of cucumber (Cucumis sativus L.) seeds during germination (ABSTRACT AVAILABLE)
Author(s): Jing HC; **vanLammeren AAM**; deCastro RD; Bino RJ; Hilhorst HWM; Groot SPC (REPRINT)
Corporate Source: CTR PLANT BREEDING & REPROD RES,AGR RES DEPT, POSTBUS 16/NL-6700 AA WAGENINGEN//NETHERLANDS/ (REPRINT); CTR PLANT BREEDING & REPROD RES,AGR RES DEPT/NL-6700 AA WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,LAB PLANT CYTOL & MORPHOL/WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,LAB PLANT PHYSIOL/WAGENINGEN//NETHERLANDS/; TIANJIN ACAD AGR SCI,/TIANJIN//PEOPLES R CHINA/
Journal: PROTOPLASMA, 1999, V208, N1-4, P230-239
ISSN: 0033-183X Publication date: 19990000
Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201 VIENNA, AUSTRIA
Language: English Document Type: ARTICLE
Abstract: Resumption of DNA synthetic activities and beta-tubulin accumulation was studied in embryo organs of germinating cucumber (Cucumis sativus L.) seeds. Flow-cytometric analysis indicated the existence of 2C, 4C, and 8C nuclei in the radicle of mature embryos, whereas in cotyledons most of the cells contained nuclei with 2C DNA content. Upon imbibition of water, nuclear DNA replication was initiated in the radicle within 15 h, subsequently spreading towards the cotyledons. Bromodeoxyuridine incorporation preceded detectable changes in the relative amounts of DNA, implying the occurrence of putative DNA repair. Organellar DNA synthesis occurred independently of the nuclear DNA synthetic cycle. Western blotting and immunohistochemical localization demonstrated that the constitutive level of beta-tubulin originated from preserved P-tubulin granules. During imbibition, disappearance of fluorescent tubulin granules, accumulation of beta-tubulin, and formation of microtubular cytoskeleton were found in the radicle, but not in the cotyledon areas. Mitosis only occurred after radicle protrusion at 21 h of imbibition. It is concluded that the differences in the initiation and progress of these cellular and molecular events are associated with the discrete behaviors of the radicle and the cotyledons upon imbibition. The formation of cortical microtubular cytoskeleton and the accumulation of tubulins are important features in preparation of radicle protrusion, whereas DNA synthesis may contribute to postgerminative growth.

15/3,AB/4 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07489949 Genuine Article#: 172TE Number of References: 53
Title: Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein kinase (ASK) multigene family (ABSTRACT AVAILABLE)
Author(s): Dornelas MC; Wittich P; vonRecklinghausen I; **vanLammeren A**; Kreis M (REPRINT)
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, ERS CNRS 569, BATIMENT 630/F-91405 ORSAY//FRANCE/ (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, ERS CNRS 569/F-91405 ORSAY//FRANCE/; AGR UNIV WAGENINGEN,LAB PLANT CYTOL & MORPHOL/NL 6703 BD WAGENINGEN//NETHERLANDS/

Journal: PLANT MOLECULAR BIOLOGY, 1999, V39, N1 (JAN), P137-147
ISSN: 0167-4412 Publication date: 19990100
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein kinase (ASK) multigene family, named ASKdzeta (ASK zeta), ASKetha (ASK eta) and ASKiota (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different ASK genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASK zeta is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.
?

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   developing embryos.
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               83  S12
                4  S13
                4  S14
                4  S15
              175  S16
     S18        0  S17 NOT S1-S16
? ds

Set      Items   Description
S1           6   ASKDZETA
S2           3   RD (unique items)
S3           0   ASK (W) DZETA NOT S1
S4          28   E1-E5
S5          12   S4 AND ARABIDOPSIS
S6           5   RD (unique items)
S7          28   E4-E9
S8           0   S7 NOT S4
S9          17   E1-E5
S10          2   S9 AND ARABIDOPSIS
S11          2   RD (unique items)
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S12          83   E3-E6
S13           4   S12 AND ARABIDOPSIS
S14           4   RD (unique items)
S15           4   S14 NOT 11
S16         175   E1-E5
S17          30   S16 AND ARABIDOPSIS
S18           0   S17 NOT S1-S16
? s s17 and ask
              30  S17
           21678  ASK
     S19       5  S17 AND ASK
? s s17 and ask?
              30  S17
          151057  ASK?
     S20       6  S17 AND ASK?
? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
 ..completed examining records
     S21       6  RD (unique items)
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>>>No matching display code(s) found in file(s): 65, 235, 306

 21/3,AB/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12473728   BIOSIS NO.: 200000227230
Arabidopsis thaliana SHAGGY-related protein kinases (AtSK11 and 12)
  function in perianth and gynoecium development.
AUTHOR: Dornelas Marcelo C; van Lammeren Andie AM; Kreis Martin(a
AUTHOR ADDRESS: (a)Institut de Biotechnologie des Plantes (IBP), UMR/CNRS
  8618, Universite de Paris-Sud, Batiment 630, F-91405, Orsay**France
JOURNAL: Plant Journal  21 (5):p419-429 March, 2000
ISSN: 0960-7412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: In higher plants, the correct patterning of the floral meristem
  in terms of organ type, number and form is the result of a concerted
  expression of a network of genes. We describe phenotypes of flower
  patterning, resulting from a reduction of transcript levels of the
  Arabidopsis SHAGGY-related protein kinase genes AtSK11(
  ASKalpha) and AtSK12(ASKalpha). The AtSK genes are plant
  homologues of the Drosophila shaggy (SGG) gene and the mammalian
  Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key
  component of the wingless signalling pathway and is required for the
  establishment of tissue patterning and cell fate determination. The
  expression patterns of the AtSK11(ASKalpha) and AtSK12(
  ASKgamma) genes during wild-type Arabidopsis inflorescence
  development, detected by in situ hybridisation, have been shown to be
  consistent with a possible role in floral meristem patterning. AtSK11(
  ASKalpha) and AtSK12(ASKgamma) transcripts were detected at
  the periphery of the inflorescence meristem and in the floral meristem.
  At later stages the expression of the AtSK genes became localised in
  specific regions of developing flower organ primordia. Furthermore, we
  have obtained and analysed transgenic plants containing AtSK11(
  ASKalpha) and AtSK12(ASKgamma) gene specific antisense
  constructs. These plants developed flowers showing a higher number of
  perianth organs and an alteration of the apical-basal patterning of the
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gynoecium.

2000

21/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11929692 BIOSIS NO.: 199900174801
Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein kinase (**ASK**) multigene family.
AUTHOR: Dornelas Marcelo Carnier; Wittich Peter; von Recklinghausen Iris; van Lammeren Andre; **Kreis Martin**(a
AUTHOR ADDRESS: (a)Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris-Sud, Batiment 630, 9140**France
JOURNAL: Plant Molecular Biology 39 (1):p137-147 Jan., 1999
ISSN: 0167-4412
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein kinase (**ASK**) multigene family, named **ASKdzeta** (**ASKzeta**), **ASKetha** (**ASKeta**) and **ASKiota** (**ASKiota**). The proteins encoded by the **ASK** genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from Drosophila and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in Drosophila. At least ten different **ASK** genes are expected to be present per haploid genome of A. thaliana. Different amino- and carboxy-terminal extensions distinguish different **ASK** family members. Five **ASK** gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five **ASK** genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While **ASKzeta** is expressed in the whole embryo during its development, **ASKeta** expression is limited to the suspensor cells. No signal was detected for **ASKalpha**, **ASKgamma** and **ASKiota** in developing embryos.

1999

21/3,AB/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11537315 BIOSIS NO.: 199800318647
The **Arabidopsis** SHAGGY-related protein kinase (**ASK**) gene family: Structure, organization and evolution.
AUTHOR: Dornelas Marcelo Carnier; Lejeune Bernard; Dron Michel; **Kreis Martin**(a
AUTHOR ADDRESS: (a)Inst. Biotechnol. Plantes, ERS/CNRS 569, Univ. Paris-Sud, Batiment 630, F-91405 Orsay Cedex**France
JOURNAL: Gene (Amsterdam) 212 (2):p249-257 June 8, 1998
ISSN: 0378-1119

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein kinase domain about 70% identical to SHAGGY protein kinase (SGG) and glycogen synthase kinase-3 (GSK-3), respectively, from Drosophila and mammals. In this study we have characterized the structure and evolution of the **Arabidopsis** SHAGGY-related protein kinase (**ASK**) gene family. At least ten **ASK** genes are present per haploid genome of **Arabidopsis**. The genomic sequences of five **ASK** genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the **Arabidopsis** gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted **ASK** genes were mapped and shown to be dispersed over the five **Arabidopsis** chromosomes. A tentative model for the organization and evolution of the **Arabidopsis ASK** genes is presented.

1998

21/3,AB/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09164576 BIOSIS NO.: 199497172946
Arabidopsis homologs of the shaggy and GSK-3 protein kinases: Molecular cloning and functional expression in Escherichia coli.
AUTHOR: Bianchi Michele W(a); Guivarc'h Dominique; Thomas Martine; Woodgett James R; **Kreis Martin**
AUTHOR ADDRESS: (a)Biol. Dev. Plantes, Centre Recherches sur les Plantes, URA 1128, Univ. Paris-Sud, Bat. 430, F-91**France
JOURNAL: Molecular & General Genetics 242 (3):p337-345 1994
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The conservation in evolution of fundamental signal transduction modules offers a means of isolating genes likely to be involved in plant development. We have amplified by PCR **Arabidopsis** cDNA and genomic sequences related to the product of the shaggy/zeste-white 3 (sgg) segment polarity gene of Drosophila. This regulatory protein is functionally homologous to glycogen synthase kinase-3 in mammals (GSK-3), which regulates, among others, the DNA-binding activity of the c-jun/AP1 transcription factor. Analysis of PCR products led to the identification of five genes; for two of which, corresponding full-length cDNAs, **ASK**-alpha and gamma (for **Arabidopsis** shaggy-related protein kinase), were characterized. The encoded proteins were 70% identical to GSK-3 and sgg over the protein kinase catalytic domain and, after production in Escherichia coli, autophosphorylated mainly on threonine and serine residues, but phosphotyrosine was also detected. **ASK**-alpha and **ASK**-gamma also phosphorylated phosphatase inhibitor-2 and myelin basic protein, on threonine and serine, respectively. The high conservation of the protein kinases of GSK-3 family, and their action at the transcriptional level, suggest that the **ASK** proteins have important functions in higher plants.

1994

21/3,AB/5 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

14249399 PASCAL No.: 99-0452372
Caracterisation d'homologues de la proteine kinase SHAGGY chez **Arabidopsis** thaliana et leur role biologique pendant le developpement
(Characterization of **Arabidopsis** thaliana homologues of SHAGGY protein kinase and their biological role during development)
DOMELAS Marcelo; **KREIS Martin**, dir
Universite de Paris 11, Orsay, Francee
Univ.: Universite de Paris 11. Orsay. FRA Degree: Th. doct.
1999-05; 1999 182 p.
Language: French Summary Language: French; English
Trois nouveaux membres de la famille multigenique **ASK** (pour **Arabidopsis** SHAGGY - related protein kinases) nommes **ASKdzeta** (**ASK** zeta), **ASKetha** (**ASK** eta) et **ASKiota** (**ASK** iota), ont ete identifies chez **Arabidopsis** thaliana. Les genes **ASK** sont des homologues vegetaux du gene SHAGGY (SGG) chez la Drosophila, appartenant a la sous-famille GSK-3 des proteines kinases. Dans un premier temps, la comparaison des sequences d'acides amines des proteines kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, evolutivement conserves, d'homologues vegetaux de SGG. La comparaison des sequences nucleotidiques des genes de la famille **ASK** a permis la proposition d'un modele d'evolution de cette famille multigenique. Par la suite, l'expression des genes **ASK** des groupes I et II a ete etudiee pendant le developpement d'**Arabidopsis** utilisant la technique d'hybridation in situ. Des plantes transgeniques contenant des constructions antisens des genes **ASK** des groupes I et II ont ete obtenues. L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les proteines **ASK** pendant le developpement floral et embryonnaire d'**Arabidopsis**.

21/3,AB/6 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

11433753 PASCAL No.: 94-0267915
Isolement et caracterisation d'homologues de la proteine kinase shaggy/GSK-3 chez **Arabidopsis** thaliana et identification d'un gene correspondant chez Saccharomyces cerevisiae
(Isolation and characterization of **Arabidopsis** thaliana homologs of the shaggy/gsk-3 protein kinase and identification of a corresponding gene in Saccharomyces cerevisiae)
BIANCHI Michele; **KREIS Martin**, dir
Universite de Paris 11, Francee
Univ.: Universite de Paris 11. FRA Degree: Th. doct.
1993-09; 1993 155 p.
Language: French Summary Language: French; English
Les proteines kinases (PKs) sont les composants centraux du systeme cybernetique des cellules eucaryotes. L'identification d'homologues de PKs conservees au cours de l'evolution peut constituer une approche complementaire aux techniques genetiques pour l'etude de voies de transduction importantes chez les plantes. Dans un premier temps, une approche de PCR (polymerase chain reaction) a permis d'identifier, chez **Arabidopsis** thaliana, une famille de genes apparentes a (1) MCK1 (meiosis and centromere regulatory kinase) de Saccharomyces cerevisiae; (2) shaggy/zeste-white 3, impliquee dans le developpement de Drosophila melanogaster; (3) le gene codant la glycogen synthase kinase-3 (GSK-3, regulateur du facteur transcriptionnel c Jun) de mammiferes. Par la suite, la caracterisation de deux ADNc, **ASK**-alpha et **ASK**-gamma (

Arabidopsis shaggy-related protein kinase), a permis de mettre en evidence une identite de 70%, au niveau du domaine catalytique, entre les proteines **ASK** et shaggy/GSK-3 dont ils representent donc les homologues vegetaux. L'activite kinase ainsi qu'une autophosphorylation sur des residus threonine, serine et, en plus faible quantite, tyrosine, ont pu etre demontrees apres production des proteines **ASK** dans E. coli. Par ailleurs, le niveau relativement faible d'identite avec MCK1 (40%) a mene a la recherche puis a l'isolement d'un deuxieme gene de S. cerevisiae: ScGSK-3, dont le produit putatif est identique a 60%, au niveau du domaine catalytique, avec GSK-3, shaggy et les proteines **ASK**. Une analyse de phylogenie moleculaire a suggere que ScGSK-3 code le veritable homologue de GSK-3 et shaggy, alors que MCK1 serait originaire d'un evenement de duplication specifique du lignage de S. cerevisiae. L'etude simultanee des PKs de la famille GSK-3 dans differents organismes devrait fournir une aide importante a la comprehension des fonctions bicchimiques et biologiques des proteines **ASK** chez les plantes superieures

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 s transform? and review? and arabidopsis
Processed  20 of  22 files ...
Processing
Completed processing all files
         1717342  TRANSFORM?
         2715044  REVIEW?
           95824  ARABIDOPSIS
      S1     315  TRANSFORM? AND REVIEW? AND ARABIDOPSIS
? s s1 and py<1998
>------User Break------>
u!
? s s1 and py>1998
Processing
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>>>  or undefined in one or more files.
Completed processing all files
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        12490415  PY>1998
      S2     144  S1 AND PY>1998
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             144  S2
          742275  VECTOR?
      S3      16  S2 AND VECTOR?
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>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
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      S4      16  RD (unique items)
? t s14/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306
>>>Set 14 does not exist
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 4,3,AB/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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13549432   BIOSIS NO.: 200200178253
Arabidopsis: A laboratory manual.
BOOK TITLE: Arabidopsis: A laboratory manual
AUTHOR: Weigel Detlef(a); Glazebrook Jane
BOOK AUTHOR/EDITOR: Weigel Detlef; Glazebrook Jane: Eds
AUTHOR ADDRESS: (a)Plant Biology Laboratory, Salk Institute, La Jolla, CA**
  USA
pp: xii; 1-354 2002
MEDIUM: print
BOOK PUBLISHER: Cold Spring Harbor Laboratory Press, 500 Sunnyside
                Boulevard, Woodbury, NY, 11797-2924, USA
ISBN: 0-87969-572-2  (cloth)
DOCUMENT TYPE: Book
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This manual contains techniques for working with
  Arabidopsis that have been assembled and reviewed by two
  members of the plant research community. In these eight chapters, the
  authors provide step-by-step guides on growth, obtaining mutants, genetic
  analysis, transforming Arabidopsis, isolating genes, studying
  gene expression and studying gene function. Each chapter includes
  bibliographical references. Appendices on where to find information,
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statistics tables, cautions, and suppliers are included. An index is also included at the back of the book.

2002

4/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

13059554 BIOSIS NO.: 200100266703
Transgenosis of **Arabidopsis** thaliana for understanding plant gene structure and functions.
AUTHOR: Ondrej Milos(a)
AUTHOR ADDRESS: (a)Institute of Plant Molecular Biology, Academy of Sciences of the Czech Republic, Branisovska 31, CZ-37005, Ceske Budejovice**Czech Republic
JOURNAL: Biologia (Bratislava) 56 (1):p1-5 February, **2001**
MEDIUM: print
ISSN: 0006 3088
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Insertion mutagenesis of **Arabidopsis** thaliana is **reviewed** as efficient means to clone genes known only by phenotype and to correlate gene sequence and function. Random insertions of T-DNA or modified maize transposons introduced into A. thaliana genome by Agrobacterium tumefaciens lead to mutations. The mutation sites are tagged by the T-DNA or modified transposon sequences and they can be cloned by plasmid rescue or iPCR. In order to have 95% probability of hitting all A. thaliana genes, 100 000 independent insertion lines should be induced and this number has already been nearly reached. Only minority of insertion mutations are connected with distinct phenotypic effect, but all insertion mutations in the chosen gene sequence can be selected by pooling insertion lines and utilization of combination of direct and reverse genetic attitudes.

2001

4/3,AB/3 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

09716323 Genuine Article#: 441TU Number of References: 199
Title: Superfluous transgene integration in plants (ABSTRACT AVAILABLE)
Author(s): Smith N (REPRINT) ; Kilpatrick JB; Whitelam GC
Corporate Source: ADAS Nutr Sci Res Unit,Alcester Rd/Stratford Upon Avon CV37 9RQ//England/ (REPRINT); ADAS Nutr Sci Res Unit,Stratford Upon Avon CV37 9RQ//England/; ADAS Rosemaund,Hereford HR1 3PG//England/; Univ Leicester,Dept Biol,Leicester LE1 7RH/Leics/England/
Journal: CRITICAL REVIEWS IN PLANT SCIENCES, **2001**, V20, N3, P215-249
ISSN: 0735-2689 Publication date: 20010000
Publisher: CRC PRESS LLC, 2000 CORPORATE BLVD NW, JOURNALS CUSTOMER SERVICE, BOCA RATON, FL 33431 USA
Language: English Document Type: REVIEW
Abstract: Recent reports suggest the transfer of superfluous DNA sequences to plant genomes during **transformation** processes. This **review** investigates the evidence from the published literature for the prevalence of this phenomenon and highlights methods to limit or prevent DNA transfer and subsequent potentially detrimental evolutionary consequences.

Evidence for superfluous foreign DNA transfer using both Agrobacterium-mediated **transformation** and direct DNA transfer methods such as microprojectile bombardment and PEG-mediated **transformation** of protoplasts is reported. In the case of Agrobacterium-mediated **transformation**, the lack of information on the integration of sequences from outside of the T-DNA borders has been due to the general belief by researchers that T-DNA processing is precise. This assumption was based on analysis of T-DNA in tumors and as a result the majority of T-DNA integration events have been identified exclusively using DNA probes, which are homologous only to DNA from within the T-DNA borders. Where direct gene transfer protocols are employed, any part of the **transforming** plasmid and indeed accompanying carrier DNA may become integrated into the plant genome. The main body of evidence proving that superfluous **vector** DNA sequences are present in plant genomes **transformed** using direct transfer methods is confined to the identification of plasmid concatamers integrated into plant genomes.

The limited amount of recorded evidence pertaining to superfluous **vector** DNA integration in transgenic plants and **transformed** tissues makes it impossible to draw definitive conclusions as to the factors involved in promoting this phenomenon. However, there are methods available for removing superfluous sequences from transgenic plants. These have been developed for the removal of selectable marker genes, whose presence in transgenic plants has been a source of much controversy, but can equally be applied to other DNA sequences. Suggestions have been made in the **review** that might limit or prevent the integration of superfluous **vector** sequences during **transformation** procedures; however, these are not proven and further research is required.

02579057 4752520
Agrobacterium-mediated plant **transformation** with large DNA fragments
Shibata, D.; Liu, Y. G.
Kazusa DNA Research Institute, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Trends in Plant Science vol. 5, no. 8, pp. 354-357 (**2000**)
ISSN: 1360-1385
DOCUMENT TYPE: Journal article; Review article LANGUAGE: ENGLISH
SUBFILE: Agricultural and Environmental Biotechnology Abstracts

Cosmid **vectors** such as pOCA18 and pLZ03 have been developed that can **transform** plants. However, the low cloning capacity of these **vectors** limits their usefulness. Recently, two research groups have developed **vectors** for the **transformation** of large DNA fragments into plants. These **vectors** are designed to have the characteristics of both bacterial artificial chromosomes (BACs) and binary **vectors** forAgrobacterium-mediated **transformation**. Therefore, large DNA fragments cloned in the T-DNA region can be transferred into a plant genome by Agrobacterium. Indeed, many genomic-DNA fragments (less than or equal to 150 kb) have been introduced successfully into several plant species by these **vectors**. This **transformation** technology has contributed to the map-based cloning (positional cloning) of novel genes defined by mutation from **Arabidopsis**. It should facilitate the isolation of dominant alleles of agronomic importance. Furthermore, the technology will be useful in plant biotechnology, especially for situations that require the simultaneous introduction of several genes, such as those encoding the enzymes of a metabolic pathway.

4/3,AB/5 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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05113757 JICST ACCESSION NUMBER: 02A0335839 FILE SEGMENT: JICST-E
Laver as a model plant in ocean and genomics.
IITSUKA OSAMU (1); KITADE YUKIHIRO (2); SAGA NAOTSUNE (2)
(1) Hokkaido Univ., Graduate School of Fisheries Sci., JPN; (2) Tokai Univ., Sch. of Mar. Sci. and Technol.
Kaiyo to Seibutsu(Aquabiology), **2002**, VOL.24,NO.1, PAGE.34-38, FIG.2, TBL.1, REF.12
JOURNAL NUMBER: S0220BAB ISSN NO: 0285-4376
UNIVERSAL DECIMAL CLASSIFICATION: 639.64 57.082 575.116.4
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Commentary
MEDIA TYPE: Printed Publication
ABSTRACT: A marine red alga Porphyra has recently received great interest not only as a valuable marine crop but also as a model plant for fundamental and applied studies in marine sciences. Porphyra has a unique dimorphic life cycle which consists of a leafy gametophytic generation and a filamentous sporophytic one. It completes its life cycle in laboratory culture within a few months and has a small number of chromosomes(2-7) in the haploid phase. The haploid genome sizes in the genus Porphyra(2.7-5.3*10^{8}bp) are in the same order of magnitude as those of **Arabidopsis** thaliana. Genetic analyses, including both classical and modern molecular studies are in progress. Now, we are performing the following subjects in order to make Porphyra a sophisticated model organism: cryo-preservation, establishment of mutant cell lines, development of host-**vector** system for **transformation**, Porphyra genome project which includes genetic map, EST, DNA macro/micro array, etc. We will introduce arrangements for an infrastructure of advanced research on Porphyra genomics which is a key to open the door toward the new marine botany world in this **review**. (author abst.)

4/3,AB/6 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04753069 H.W. WILSON RECORD NUMBER: BGSA02003069
Staminodes: their morphological and evolutionary significance.
Ronse Decraene, L. P
Smets, E. F
The Botanical Review (Bot Rev) v. 67 no3 (July/Sept. 2001) p. 351-402
SPECIAL FEATURES: bibl il tab ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 20563

4/3,AB/7 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2002 The HW Wilson Co. All rts. reserv.

04751956 H.W. WILSON RECORD NUMBER: BGSA02001956
Biology of mammalian L1 retrotransposons.
Ostertag, Eric M
Kazazian, Haig H
Annual Review of Genetics v. 35 (2001) p. 501-38
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English

COUNTRY OF PUBLICATION: United States
WORD COUNT: 18786

ABSTRACT: L1 retrotransposons comprise 17% of the human genome. Although most L1s are inactive, some elements remain capable of retrotransposition. L1 elements have a long evolutionary history dating to the beginnings of eukaryotic existence. Although many aspects of their retrotransposition mechanism remain poorly understood, they likely integrate into genomic DNA by a process called target primed reverse transcription. L1s have shaped mammalian genomes through a number of mechanisms. First, they have greatly expanded the genome both by their own retrotransposition and by providing the machinery necessary for the retrotransposition of other mobile elements, such as Alus. Second, they have shuffled non-L1 sequence throughout the genome by a process termed transduction. Third, they have affected gene expression by a number of mechanisms. For instance, they occasionally insert into genes and cause disease both in humans and in mice. L1 elements have proven useful as phylogenetic markers and may find other practical applications in gene discovery following insertional mutagenesis in mice and in the delivery of therapeutic genes. Reprinted by permission of the publisher.

4/3,AB/3 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04504719 H.W. WILSON RECORD NUMBER: BGSA01004719
Recognition and silencing of repeated DNA.
Hsieh, Jenny
Fire, Andrew
Annual Review of Genetics v. 34 (2000) p. 187-204
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8041

ABSTRACT: Mechanisms for repetition of DNA pose both opportunities and challenges to a functional genome: opportunities for increasing gene expression by amplification of useful sequences, and challenges of controlling amplification by unwanted sequences such as transposons and viruses. Experiments in numerous organisms have suggested the likely existence of a general mechanism for recognition of repeated character in DNA. This **review** focuses (a) on the nature of these recognition mechanisms, and (b) on types of chromatin modification and gene silencing that are used to control repeated DNA. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

4/3,AB/4 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04202907 H.W. WILSON RECORD NUMBER: BGSA00022907
Mercury toxicity in plants.
Patra, Manomita
Sharma, Archana
The Botanical Review (Bot Rev) v. 66 no3 (July/Sept. 2000) p. 379-422
SPECIAL FEATURES: bibl il tab ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 25426

ABSTRACT: Mercury poisoning has become a problem of current interest as a result of environmental pollution on a global scale. Natural emissions of

mercury form two-thirds of the input; manmade releases form about one-third. Considerable amounts of mercury may be added to agricultural land with sludge, fertilizers, lime, and manures. The most important sources of contaminating agricultural soil have been the use of organic mercurials as a seed-coat dressing to prevent fungal diseases in seeds. In general, the effect of treatment on germination is favorable when recommended dosages are used. Injury to the seed increases in direct proportion to increasing rates of application. The availability of soil mercury to plants is low, and there is a tendency for mercury to accumulate in roots, indicating that the roots serve as a barrier to mercury uptake. Mercury concentration in aboveground parts of plants appears to depend largely on foliar uptake of Hg0 volatilized from the soil. Uptake of mercury has been found to be plant specific in bryophytes, lichens, wetland plants, woody plants, and crop plants. Factors affecting plant uptake include soil or sediment organic content, carbon exchange capacity, oxide and carbonate content, redox potential, formulation used, and total metal content. In general, mercury uptake in plants could be related to pollution level. With lower levels of mercury pollution, the amounts in crops are below the permissible levels. Aquatic plants have shown to be bioaccumulators of mercury. Mercury concentrations in the plants (stems and leaves) are always greater when the metal is introduced in organic form. In freshwater aquatic vascular plants, differences in uptake rate depend on the species of plant, seasonal growth-rate changes, and the metal ion being absorbed. Some of the mercury emitted from the source into the atmosphere is absorbed by plant leaves and migrates to humus through fallen leaves. Mercury-vapor uptake by leaves of the C3 species oats, barley, and wheat is five times greater than that by leaves of the C4 species corn, sorghum, and crabgrass. Such differential uptake by C3 and C4 species is largely attributable to internal resistance to mercury-vapor binding. Airborne mercury thus seems to contribute significantly to the mercury content of crops and thereby to its intake by humans as food. Accumulation, toxicity response, and mercury distribution differ between plants exposed through shoots or through roots, even when internal mercury concentrations in the treated plants are similar. Throughfall and litterfall play a significant role in the cycling and deposition of mercury. The possible causal mechanisms of mercury toxicity are changes in the permeability of the cell membrane, reactions of sulphydryl (-SH) groups with cations, affinity for reacting with phosphate groups and active groups of ADP or ATP, and replacement of essential ions, mainly major cations. In general, inorganic forms are thought to be more available to plants than are organic ones. Reprinted by permission of the publisher.

04265194 H.W. WILSON RECORD NUMBER: BGSA00015194
LEAFY and the evolution of rosette flowering in violet cress (Jonopsidium acaule, Brassicaceae).
Shu, Guoping
Amaral, Weber; Hileman, Lena C
American Journal of Botany v. 87 no5 (May 2000) p. 634-41
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5493

ABSTRACT: **Arabidopsis** and most other Brassicaceae produce an elongated inflorescence of mainly ebracteate flowers. However, the early-flowering species violet cress (Jonopsidium acaule) and a handful of other species produce flowers singly in the axils of rosette leaves. In **Arabidopsis** the gene LEAFY (LFY) is implicated in both the determination of flower meristem identity and in the suppression of leaves

(bracts) that would other wise subtend the flowers. In this study we examined the role of LFY homologs in the evolution of rosette flowering in violet cress. We cloned two LFY homologs, vcLFY1 and vcLFY2, from violet cress. Their exon sequences show U90% nucleotide similarity with **Arabidopsis** LFY and 99% similarity to each other. We used in situ hybridization to study vcLFY expression in violet cress. The patterns were very similar to LFY in **Arabidopsis** except for stronger expression in the shoot apical meristem outside of the region of flower meristem initiation. It is possible that the relatively diffuse expression of vcLFY contributes to the lack of bract suppression in violet cress. Additionally, the earliest flowers produced by violet cress express vcLFY, suggesting that accelerated flowering in violet cress could also result from changes in the regulation of vcLFY. Reprinted by permission of the publisher.

4/3,AB/11 (Item 6 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04264504 H.W. WILSON RECORD NUMBER: BGSA00014504
Crown gall disease and Agrobacterium tumefaciens: a study of the history, present knowledge, missing information, and impact on molecular genetics.
Stafford, Helen A
The Botanical Review (Bot Rev) v. 66 no1 (Jan./Mar. 2000) p. 99-118
SPECIAL FEATURES: bibl il ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10929

ABSTRACT: The production of crown gall tumors in plants caused by Agrobacterium tumefaciens represents a unique disease involving the transfer of DNA from the bacterium to the nucleus of the plant. Vital aspects of this transfer are still being studied. Reprinted by permission of the publisher.

4/3,AB/12 (Item 7 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04255640 H.W. WILSON RECORD NUMBER: BGSA00005640
Plant retrotransposons.
AUGMENTED TITLE: **review**
Kumar, Amar
Bennetzen, Jeffrey L
Annual Review of Genetics v. 33 (1999) p. 479-532
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 22407

ABSTRACT: Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in plants and play a major role in plant gene and genome evolution. In many cases, retrotransposons comprise over 50% of nuclear DNA content, a situation that can arise in just a few million years. Plant retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in plants compared to some other eukaryotes, including their often-high copy numbers, their extensively heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This

review describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to plant genome evolution and their use as genetic tools in plant biology. Reprinted by permission of the publisher.

4/3,AB/13 (Item 8 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04255140 H.W. WILSON RECORD NUMBER: BGSA00005140
Phylogenetic structure in the grass family (Poaceae): evidence from the nuclear gene phytochrome B.
Mathews, Sarah
Tsai, Rocky C; Kellogg, Elizabeth A
American Journal of Botany v. 87 no1 (Jan. 2000) p. 96-107
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8359

ABSTRACT: Phylogenetic analyses of partial phytochrome B (PHYB) nuclear DNA sequences provide unambiguous resolution of evolutionary relationships within Poaceae. Analysis of PHYB nucleotides from 51 taxa representing seven traditionally recognized subfamilies clearly distinguishes three early-diverging herbaceous "bambusoid" lineages. First and most basal are Anomochloa and Streptochaeta, second is Pharus, and third is Puelia. The remaining grasses occur in two principal, highly supported clades. The first comprises bambusoid, oryzoid, and pooid genera (the BOP clade); the second comprises panicoid, arundinoid, chloridoid, and centothecoid genera (the PACC clade). The PHYB phylogeny is the first nuclear gene tree to address comprehensively phylogenetic relationships among grasses. It corroborates several inferences made from chloroplast gene trees, including the PACC clade, and the basal position of the herbaceous bamboos Anomochloa, Streptochaeta, and Pharus. However, the clear resolution of the sister group relationship among bambusoids, oryzoids, and pooids in the PHYB tree is novel: the relationship is only weakly supported in ndhF trees and is nonexistent in rbcL and plastid restriction site trees. Nuclear PHYB data support Anomochlooideae, PHaroideae, Pooideae sensu lato, Oryzoideae, Panicoideae, and Chloridoideae, and concur in the polyphyly of both Arundinoideae and Bambusoideae. Reprinted by permission of the publisher.

4/3,AB/14 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04045904 H.W. WILSON RECORD NUMBER: BGSI99045904
Cellular and molecular biology of the aquaporin water channels.
Borgnia, Mario
Nielsen, S ren; Engel, Andreas
Annual Review of Biochemistry v. 68 (1999) p. 425-58
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12474

ABSTRACT: The high water permeability characteristic of mammalian red cell membranes is now known to be caused by the protein AQP1. This channel freely permits movement of water across the cell membrane, but it is not permeated by other small, uncharged molecules or charged solutes. AQP1 is a tetramer with each subunit containing an aqueous pore likened to an hourglass formed by oppositely arranged tandem repeats. Cryoelectron microscopy of reconstituted AQP1 membrane crystals has revealed the

three-dimensional structure at 3-6 A. AQP1 is distributed in apical and basolateral membranes of renal proximal tubules and descending thin limbs as well as capillary endothelia. Ten mammalian aquaporins have been identified in water-permeable tissues and fall into two groupings. Orthodox aquaporins are water-selective and include AQP2, a vasopressin-regulated water channel in renal collecting duct, in addition to AQP0, AQP4, and AQP5. Multifunctional aquaglyceroporins AQP3, AQP7, and AQP9 are permeated by water, glycerol, and some other solutes. Aquaporins are being defined in numerous other species including amphibia, insects, plants, and microbials. Members of the aquaporin family are implicated in numerous physiological processes as well as the pathophysiology of a wide range of clinical disorders. Reprinted by permission of the publisher.

4/3,AB/15 (Item 10 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04014401 H.W. WILSON RECORD NUMBER: BGSI99014401
Heat-shock proteins, molecular chaperones, and the stress response: evolutionary and ecological physiology.
AUGMENTED TITLE: **review**
Feder, Martin E
Hofmann, Gretchen E
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82
SPECIAL FEATURES: bibl il ISSN: 0066-4278
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual **Review** of Physiology, Volume 61, 1999, by Annual **Reviews** Inc. (http://www.annurev.org).

4/3,AB/16 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
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0242901 DBA Accession No.: 1999-13566
Towards molecular farming in the future: using plant-cell-suspension cultures as bioreactors - for example **vector**-mediated tobacco transgenic plant construction, used for recombinant antibody, protein production, etc. **review**
AUTHOR: Fischer R; Emans N; Schuster F; Hellwig S; Drossard J
CORPORATE AFFILIATE: Tech.Coll.Aachen-Inst.Biol.

Inst.Environ.Chem.Ecotox.Schmallenberg
CORPORATE SOURCE: Institut fuer Biologie, RWTH Aachen, Worringerweg 1, D-52074 Aachen, Germany.
JOURNAL: Biotechnol.Appl.Biochem. (30, Pt.2, 109-12) **1999**
ISSN: 0885-4513 CODEN: BABIEC
LANGUAGE: English
ABSTRACT: Plant-suspension cells are **reviewed** as an in vitro system for the production of recombinant protein under carefully controlled certified conditions. Free cell suspensions are considered to be the most suitable for large-scale applications in the biotechnology industry. Plant species used for generation and propagation of suspension cell cultures include **Arabidopsis** sp., Catharanthus sp., yew (Taxus sp.), rice (Oryza sativa), soybean Glycine max), alfalfa (Medicago sativa) and tobacco (Nicotiana tabacum). Plant cell suspensions can be cultivated in shake flasks or culture vessel using batch, fed-batch, perfusion and continuous culture. For recombinant protein production Agrobacterium sp.-mediated **transformation**, microparticle bombardment, electroporation of protoplasts or virus **vectors** can all be used. Tobacco suspension cell cultures have been used to express IgGs, Fab fragments, single chains, bispecific antibody fragments and fusion proteins. Tobacco BY-2 cells have been used for culture using a working volume of 40 l. A 10% (v/v) inoculum with a culture time of 150 hr produced a yield of 7.5 kg fresh cell weight. (52 ref)

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          229288  POTATO
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           93591  BEET
           60469  SUGAR(W)BEET
          490457  SUGAR
           52728  CANE
           29533  SUGAR(W)CANE
          397838  RICE
          366124  MAIZE
          239324  BARLEY
          582106  WHEAT
         1717342  TRANSFORM?
          742275  VECTOR?
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         2715044  REVIEW?
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>>>No matching display code(s) found in file(s): 65, 235, 306

 8/3,AB/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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13164582   BIOSIS NO.: 200100371731
Genetic transformation of wheat: Progress during the 1990s into
  the Millennium.
AUTHOR: Ingram Heidi M; Livesey Nancy L; Power J Brian; Davey Michael R(a)
AUTHOR ADDRESS: (a)Plant Science Division, School of Biosciences,
  University of Nottingham, University Park, Nottingham, NG7 2RD**UK
JOURNAL: Acta Physiologiae Plantarum  23 (2):p221-239 2001
MEDIUM: print
ISSN: 0137-5881
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT  Wheat transformation technology has progressed
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rapidly during the past decade. Initially, procedures developed for protoplast isolation and culture, electroporation- and polyethylene glycol (PEG)-induced DNA transfer enabled foreign genes to be introduced into **wheat** cells. The development of biolistic (microprojectile) bombardment procedures led to a more efficient approach for direct gene transfer. More recently, Agrobacterium-mediated gene delivery procedures, initially developed for the **transformation** of **rice**, have also been used to generate transgenic **wheat** plants. This **review** summarises the considerable progress in **wheat transformation** achieved during the last decade. An increase in food production is essential in order to sustain the increasing world population. This could be achieved by the development of higher yielding varieties with improved nutritional quality and tolerance to biotic and abiotic stresses. Although conventional breeding will continue to play a major role in increasing crop yield, laboratory-based techniques, such as genetic **transformation** to introduce novel genes into crop plants, will be essential in complementing existing breeding technologies. A decade ago, cereals were considered recalcitrant to **transformation**. Since then, a significant research effort has been focused on cereals because of their agronomic status, leading to improved genetic **transformation** procedures (Bommineni and Jauhar 1997). Initially, the genetic **transformation** of cereals relied on the introduction of DNA into protoplasts and the subsequent production of callus from which fertile plants were regenerated. More recently, major advances have been accomplished in the regeneration of fertile plants from a range of source tissues, providing an essential foundation for the generation of transgenic plants. This **review** summarises procedures, **vectors** and target tissues used for **transformation**, highlights the limitations of current approaches and discusses future trends. The citation of references is limited, where possible, to the most relevant or recent reports.

2001

8/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13059554 BIOSIS NO.: 200100266703
Transgenosis of Arabidopsis thaliana for understanding plant gene structure and functions.
AUTHOR: Ondrej Milos(a)
AUTHOR ADDRESS: (a)Institute of Plant Molecular Biology, Academy of Sciences of the Czech Republic, Branisovska 31, CZ-37005, Ceske Budejovice**Czech Republic
JOURNAL: Biologia (Bratislava) 56 (1):p1-5 February, **2001**
MEDIUM: print
ISSN: 0006-3088
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Insertion mutagenesis of Arabidopsis thaliana is **reviewed** as efficient means to clone genes known only by phenotype and to correlate gene sequence and function. Random insertions of T-DNA or modified **maize** transposons introduced into A. thaliana genome by Agrobacterium tumefaciens lead to mutations. The mutation sites are tagged by the T-DNA or modified transposon sequences and they can be cloned by plasmid rescue or iPCR. In order to have 95% probability of hitting all A. thaliana genes, 100 000 independent insertion lines should be induced and this number has already been nearly reached. Only minority of insertion mutations are connected with distinct phenotypic effect, but

all insertion mutations in the chosen gene sequence can be selected by pooling insertion lines and utilization of combination of direct and reverse genetic attitudes.

2001

8/3,AB/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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12489958 BIOSIS NO.: 200000239460
Agrobacterium-mediated **transformation** of cereals: From technique development to its application.
AUTHOR: Nadolska-Orczyk Anna(a); Orczyk Waclaw(a); Przetakiewicz Anna(a)
AUTHOR ADDRESS: (a)Department of Biotechnology and Cytogenetics, Plant Breeding and Acclimatization Institute, 05-870, Blonie**Poland
JOURNAL: Acta Physiologiae Plantarum 22 (1):p77-88 **2000**
ISSN: 0137-5881
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Agrobacterium tumefaciens is a very useful **vector** to transfer foreign genes into dicotyledonous cells. Monocotyledonous, especially cereals, were considered outside the host range of the bacteria. The main, alternative technique of **transformation** developed for them was delivery of naked DNA (e.g. micro-projectile bombardment, electroporation of protoplasts). The results of Agrobacterium-mediated **transformation** of cereals accumulated during the last few years confirmed that the method was reliable and repeatable also for this group of plants. The most important advantages of Agro-based system include relatively high **transformation** efficiency, integration of defined piece of DNA (transgene) frequently as a single copy, Mendelian transmission to the next generation, simple **transformation** procedure and lower cost of equipment than biolistic. Discussed are the crucial factors of successful Agrobacterium-mediated **transformation** of cereals: type of plant tissue used, A. tumefaciens strains and plasmids (**vectors**), activation of bacterial virulence system and promoter, reporter as well as selectable genes applied for transgene construction. The **review** contains examples of Agrobacterium-based **transformation** methods and practical opportunities of their application as well as the list and description of cereal transgenic plants (**rice**, **maize**, **wheat** and **barley**) obtained after Agrobacterium-mediated **transformation**.

2000

8/3,AB/4 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

10258424 Genuine Article#: 505DZ Number of References: 178
Title: Invited **review**: Use of Ri-mediated **transformation** for production of transgenic plants (ABSTRACT AVAILABLE)
Author(s): Christey MC (REPRINT)
Corporate Source: Crop & Food Res,Private Bag 4704/Christchurch//New Zealand/ (REPRINT); Crop & Food Res,Christchurch//New Zealand/
Journal: IN VITRO CELLULAR & DEVELOPMENTAL BIOLOGY-PLANT, **2001**, V37, N6 (NOV-DEC), P687-700
ISSN: 1054-5476 Publication date: 20011100

Publisher: C A B I PUBLISHING, C/O PUBLISHING DIVISION, WALLINGFORD OX10 8DE, OXON, ENGLAND
Language: English Document Type: REVIEW
Abstract: Agrobacterium rhizogenes-mediated **transformation** has been used to obtain transgenic plants in 89 different taxa, representing 79 species from 55 genera and 27 families. A diverse range of dicotyledonous plant families is represented, including one Gymnosperm family. In addition to the Ri plasmid, over half these plants have been **transformed** with foreign genes, including agronomically useful traits. Plants regenerated from hairy roots often show altered plant morphology such as dwarfing, increased rooting, altered flowering, wrinkled leaves and/or increased branching due to rol gene expression. These altered phenotypic features can have potential applications for plant improvement especially in the horticultural industry where such morphological alterations may be desirable. Use of A. rhizogenes and rol gene **transformation** has tremendous potential for genetic manipulation of plants and has been of particular benefit for improvement of ornamental and woody plants.

8/3,AB/5 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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09719323 Genuine Article#: 441TU Number of References: 199
Title: Superfluous transgene integration in plants (ABSTRACT AVAILABLE)
Author(s): Smith N (REPRINT) ; Kilpatrick JB; Whitelam GC
Corporate Source: ADAS Nutr Sci Res Unit,Alcester Rd/Stratford Upon Avon CV37 9RQ//England/ (REPRINT); ADAS Nutr Sci Res Unit,Stratford Upon Avon CV37 9RQ//England/; ADAS Rosemaund,Hereford HR1 3PG//England/; Univ Leicester,Dept Biol,Leicester LE1 7RH,Leics,England/
Journal: CRITICAL REVIEWS IN PLANT SCIENCES, **2001**, V20, N3, P215-249
ISSN: 0735-2689 Publication date: 20010000
Publisher: CRC PRESS LLC, 2000 CORPORATE BLVD NW, JOURNALS CUSTOMER SERVICE, BOCA RATON, FL 33431 USA
Language: English Document Type: REVIEW
Abstract: Recent reports suggest the transfer of superfluous DNA sequences to plant genomes during **transformation** processes. This **review** investigates the evidence from the published literature for the prevalence of this phenomenon and highlights methods to limit or prevent DNA transfer and subsequent potentially detrimental evolutionary consequences.

Evidence for superfluous foreign DNA transfer using both Agrobacterium-mediated **transformation** and direct DNA transfer methods such as microprojectile bombardment and PEG-mediated **transformation** of protoplasts is reported. In the case of Agrobacterium-mediated **transformation**, the lack of information on the integration of sequences from outside of the T-DNA borders has been due to the general belief by researchers that T-DNA processing is precise. This assumption was based on analysis of T-DNA in tumors and as a result the majority of T-DNA integration events have been identified exclusively using DNA probes, which are homologous only to DNA from within the T-DNA borders. Where direct gene transfer protocols are employed, any part of the **transforming** plasmid and indeed accompanying carrier DNA may become integrated into the plant genome. The main body of evidence proving that superfluous **vector** DNA sequences are present in plant genomes **transformed** using direct transfer methods is confined to the identification of plasmid concatamers integrated into plant genomes.

The limited amount of recorded evidence pertaining to superfluous **vector** DNA integration in transgenic plants and **transformed** tissues makes it impossible to draw definitive conclusions as to the

factors involved in promoting this phenomenon. However, there are methods available for removing superfluous sequences from transgenic plants. These have been developed for the removal of selectable marker genes, whose presence in transgenic plants has been a source of much controversy, but can equally be applied to other DNA sequences. Suggestions have been made in the **review** that might limit or prevent the integration of superfluous **vector** sequences during **transformation** procedures; however, these are not proven and further research is required.

8/3,AB/6 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03985377 CAB Accession Number: 20003003941
Resistance and tolerance to **barley** yellow dwarf in cereals: new perspectives.
Barbieri, R. L.; Oliveira, A. C. de; Carvalho, F. I. F. de
Departamento de Fitotecnia, Universidade Federal de Pelotas, Caixa Postal 354, 96001.970, RS, Brazil.
Journal of New Seeds vol. 2 (2): p.23-35
Publication Year: 2000
ISSN: 1522-886X --
Language: English
Document Type: Journal article
Barley yellow dwarf is a cereal virus disease transmitted by aphids. It is an important factor of yield losses for all cereals, including **wheat**, **barley** , oat and triticale. It is caused by related viruses known as BYDVs, members of the Luteoviridae family. Selection for resistance and tolerance to BYDVs is not an easy task to accomplish in breeding programs, because they suffer high environmental influence. In the last years, biotechnology has presented some approaches to complement traditional breeding programmes. These include identification of molecular markers linked to resistance and tolerance genes, in order to make possible marker assisted selection, and **transformation** of hosts with genes conferring resistance to BYDVs. 55 ref.

8/3,AB/7 (Item 2 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03811610 CAB Accession Number: 991612352
Wheat starch modification through biotechnology.
Baga, M.; Repellin, A.; Demeke, T.; Caswell, K.; Leung, N.; Abdel-Aal, E. S.; Hucl, P.; Chibbar, R. N.
Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon S7N 0W9, Canada.
Starch/Starke vol. 51 (4): p.111-116
Publication Year: 1999
ISSN: 0038-9056 --
Language: English
Document Type: Journal article
Natural mutations that affect the amylose/amylopectin ratio in starch are unlikely to develop naturally in **wheat** due to its allohexaploid genome (2n = 6x; AABBDD). Biotechnological techniques to modify **wheat** starch are **reviewed**. One of the strategies to modify **wheat** starch structure involves identification of germplasms with null alleles for starch biosynthetic genes, followed by exchange of functional alleles with the identified null alleles through classical plant breeding. This technique has successfully been used to combine the three null alleles for granule bound starch synthase 1 to develop a

wheat line that produces amylopectin-rich (>95%) starch (waxy starch). Another strategy to alter expression levels of starch biosynthetic genes employs recent advances in molecular biology and genetic engineering of **wheat** . For this approach, various monocotyledon **vectors** have been developed that drive expression of **wheat** starch branching enzyme I (SBEI) cDNA sequences in the anti-sense orientation. Several of the **wheat** cell lines **transformed** with the anti-sense **vectors** express branching enzyme (BE) activity at a significantly lower level than non-**transformed** cells. One transgenic **wheat** plant expressing the anti-sense SBEI RNA produces a 10-fold lower level of BE activity in kernels than wild-type **wheat**. Analysis of starch produced from the transgenic plant shows that starch structure and properties have been altered. 57 ref.

8/3,AB/8 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04835490 H.W. WILSON RECORD NUMBER: BGSA02185490
Poverty and environmental degradation: challenges within the global economy.
Mabogunje, Akin L
Environment v. 44 no1 (Jan./Feb. 2002) p. 8-18
SPECIAL FEATURES: bibl f il ISSN: 0013-9157
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7558

ABSTRACT: The challenges of dealing with poverty and environmental degradation within the context of the global economy are discussed. Deepening poverty and environmental degradation are linked, and since the end of the Second World War, the visibility and extent of both of these phenomena has increased. This has occurred in spite of the efforts of the UN and related international agencies to promote global development in a series of well-publicized social and economic development efforts. Globalization is perhaps the single most important development in the world today. Although it exacerbates poverty in some places and among some groups, globalization also has a democratizing potential that may be essential to breaking out of poverty.

8/3,AB/9 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04857477 H.W. WILSON RECORD NUMBER: BGSA02107477
A waterborne outbreak of Escherichia coli O157:H7 infections and hemolytic uremic syndrome: implications for rural water systems.
Olsen, Sonja J
Miller, Gayle; Breuer, Thomas
Emerging Infectious Diseases (Emerging Infect Dis) v. 8 no4 (Apr. 2002) p. 370-5
SPECIAL FEATURES: bibl f graph tab ISSN: 1080-6040
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 4577

8/3,AB/10 (Item 3 from file: 98)
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04857260 H.W. WILSON RECORD NUMBER: BGSA02107260
Role of gravity waves in triggering deep convection during TOGA COARE
Lac, C
Lafore, J.-P; Redelsperger, J.-L
Journal of the Atmospheric Sciences (J Atmos Sci) v. 59 no8 (Apr. 15 2002) p. 1293-316
SPECIAL FEATURES: bibl graph il ISSN: 0022-4928
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10971

ABSTRACT: The role of gravity waves in the initiation of convection over oceanic regions during the Tropical Ocean Global Atmosphere Coupled Ocean-Atmosphere Response Experiment (TOGA COARE) experiment is investigated. First, an autocorrelation method is applied to infrared temperature observations of convective events from satellite images. It reveals that new deep convective cells often occur a few hours after a previous intense event at a typical distance of a few hundred kilometers. Such fast moving modes (faster than 15 m s-1) are interpreted as the trace of gravity waves excited by previous convection and contributing to trigger further convection. Second, the specific case of 11-12 December 1992, during which an active squall line is generated after the collapse of a previous mesoscale convective system (MCS) nearby, is analyzed with a nonhydrostatic model. The triggering of the second MCS is well reproduced explicitly, owing to the use of the two-way interactive grid nesting. The convective source appears to emit pulses of gravity waves on a wide range of small scales. On the contrary, the troposphere response to the convective source exhibits a spectral simplicity. A slowly evolving mode, characterized by an ascent in the PBL and a compensating subsidence in the free troposphere, favors shallow convection and inhibits deep convection, respectively. Traveling modes propagating away from the convective source are characterized by a fast mode ({similar}50 m s-1) and a slower mode ({similar}25 m s-1) associated with the convective and stratiform development of the source, respectively, in agreement with previous studies. A budget analysis reveals the different factors leading to the deep convection triggering. First, an active PBL characterized by strong surface fluxes and mean ascent, initiates shallow convection, lasting about 2 h, inhibited above by the subsiding motions maintaining a dry layer. Second, horizontal advection of moist and cooler air at midlevels, and detrainment from cumuli, contribute to destroy the dry air layer capping the shallow convective layer. Finally, vertical advection induced by the gravity waves passage modulates the vapor and temperature evolution. Ascending phases favor moistening and cooling, whereas subsiding phases stop these effects, delaying the deep convection onset. The triggering occurs after a strong subsidence, when the ascent phases of deep and shallow modes are combined. Reprinted by permission of the publisher.

8/3,AB/11 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04693824 H.W. WILSON RECORD NUMBER: BGSA02103824
Predicting the risk of Lyme disease: habitat suitability for Ixodes scapularis in the north central United States.
Guerra, Marta
Walker, Edward; Jones, Carl
Emerging Infectious Diseases (Emerging Infect Dis) v. 8 no3 (Mar. 2002) p. 289-97
SPECIAL FEATURES: bibl f graph il map tab ISSN: 1080-6040
LANGUAGE English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7085

ABSTRACT: The distribution and abundance of Ixodes scapularis were studied in Wisconsin, northern Illinois, and portions of the Upper Peninsula of Michigan by inspecting small mammals for ticks and by collecting questing ticks in state parks and natural areas. Environmental data were gathered at a local level (i.e., micro and meso levels), and a geographic information system (GIS) was used with several digitized coverages of environmental data to create a habitat profile for each site and a grid map for Wisconsin and Illinois. Results showed that the presence and abundance of I. scapularis varied, even when the host population was adequate. Tick presence was positively associated with deciduous, dry to mesic forests and alfisol-type soils of sandy or loam-sand textures overlying sedimentary rock. Tick absence was associated with grasslands, conifer forests, wet to wet/mesic forests, acidic soils of low fertility and a clay soil texture, and Precambrian bedrock. We performed a discriminant analysis to determine environmental differences between positive and negative tick sites and derived a regression equation to examine the probability of I. scapularis presence per grid. Both analyses indicated that soil order and land cover were the dominant contributors to tick presence. We then constructed a risk map indicating suitable habitats within areas where I. scapularis is already established. The risk map also shows areas of high probability the tick will become established if introduced. Thus, this risk analysis has both explanatory power and predictive capability. Reprinted by permission of the publisher.

8/3,AB/12 (Item 5 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04851481 H.W. WILSON RECORD NUMBER: BGSA02101481
Ambient air pollution and risk of birth defects in southern California.
Ritz, Beate
Yu, Fei; Fruin, Scott
American Journal of Epidemiology (Am J Epidemiol) v. 155 no1 (Jan. 1 2002)
p. 17-25
SPECIAL FEATURES: bibl f tab ISSN: 0002-9262
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5979

ABSTRACT: The authors evaluated the effect of air pollution on the occurrence of birth defects ascertained by the California Birth Defects Monitoring Program in neonates and fetuses delivered in southern California in 1987-1993. By using measurements from ambient monitoring stations of carbon monoxide (CO), nitrogen dioxide, ozone, and particulate matter <10 mm in aerodynamic diameter, they calculated average monthly exposure estimates for each pregnancy. Conventional, polytomous, and hierarchical logistic regression was used to estimate odds ratios for subgroups of cardiac and orofacial defects. Odds ratios for cardiac ventricular septal defects increased in a dose-response fashion with increasing second-month CO exposure (odds ratio (OR)2nd quartile CO = 1.62, 95% confidence interval (CI): 1.05, 2.48; OR3rd quartile CO = 2.09, 95% CI: 1.19, 3.67; OR4th quartile CO = 2.95, 95% CI: 1.44, 6.05). Similarly, risks for aortic artery and valve defects, pulmonary artery and valve anomalies, and conotruncal defects increased with second-month ozone exposure. The study was inconclusive for other air pollutants. The authors' results are supported by the specificity of the timing of the effect and some evidence from animal data; however, this is the first known study to link ambient air pollution during a vulnerable window of development to human malformations. Confirmation by further studies is needed. Reprinted by permission of the publisher.

8/3,AB/13 (Item 6 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text
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04756169 H.W. WILSON RECORD NUMBER: BGSA02006169
Madagasikaria (Malpighiaceae): a new genus from Madagascar witih implications for floral evolution in Malpighiaceae.
Davis, Charles C
American Journal of Botany (Am J Bot) v. 89 no4 (Apr. 2002) p. 699-706
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5899

ABSTRACT: Madagasikaria andersonii is described here as a new genus and species of Malpighiaceae from Madagascar. The phylogenetic placement of Madagasikaria was estimated by using combined data from ndhF and trnL-F chloroplast sequences and phytochrome (PHYC) and ITS nuclear sequences. It forms a strongly supported clade with the Malagasy endemic genera Rhynchophora and Microsteira. Despite nearly identical floral morphology among species in this clade (here called the madagasikarioid clade), these genera are easily distinguishable on the basis of their fruits. The schizocarpic fruits of Madagasikaria have distinctive mericarps. Each mericarp has a lateral wing, which completely encircles the nut, and a peculiar dorsal wing, which folds over on itself. The morphology of this fruit suggests that the homology of the unusual wing in Rhynchophora is lateral in nature and represents a reduced wing similar to the lateral wing in Madagasikaria. Taxa in the madagasikaricid clade all appear to be morphologically androdioecious and functionally dioecious, producing both staminate and "bisexual" (i.e., functionally carpellate) individuals. This condition appears to be exceedingly rare in flowering plants and has important implications for floral evolution within Malpighiaceae. Neotropical Malpighiaceae are pollinated by specialized oil-collecting anthophorine bees of the tribe Centridini and exhibit highly conserved floral morphology despite tremendous diversity in fruit morphology and habit. These oil-collecting bees are absent from the paleotropics, where most members of the Malpighiaceae lack both the oil glands and the typical floral orientation crucial to pollination by neotropical oil-collecting bees. The madagasikarioids represent one shift from the neotropical pollination syndrome among Old World Malpighiaceae. Reprinted by permission of the publisher.

9/3,AB/14 (Item 7 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04754361 H.W. WILSON RECORD NUMBER: BGSA02004361
The use of DNA sequencing (ITS and trnL-F), AFLP, and fluorescent in situ hybridization to study allopolyploid Miscanthus (Poaceae).
Hodkinson, Trevor R
Hase, Mark W; Takahashi, Chigusa
American Journal of Botany (Am J Bot) v. 89 no2 (Feb. 2002) p. 279-86
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6937

ABSTRACT. Two clones of Miscanthus, grown under the names M. Xgiganteus and M. sacchariflorus, have been used in biomass trials in Europe, but neither the identity of these clones nor their origin has been established. DNA sequencing, amplified fragment length polymorphism (AFLP), and chromosome studies confirm that M. Xgiganteus is an allotriploid (2n = 3x = 57) combining genomes from M. sinensis (2n = 2x = 38) and M. sacchariflorus (2n = 38 or 76). Two alleles of the internal transcribed spacer of 18S-25S

nuclear ribosomal DNA (ITS) were discovered in polymerase chain reaction products of M. Xgiganteus. Cloning of these revealed that one matched M. sinensis and the other M. sacchariflours. Plastid trnL intron and trnL-F spacer sequences showed that the maternal lineage of M. Xgiganteus was M. sacchariflorus. Fluorescent in situ hybridization. FISH, was used to investigate genome organization in Miscanthus but was unable to differentiate between the different parental genomes present in M. Xgiganteus, indicating that two parental genomes are still extremely similar at the repetitive DNA level. This study is an example in which rDNA sequences and AFLP fingerprints permit identification of the parental genomes in a hybrid, but FISH methods, at the repetitive DNA level (including genomic in situ hybridization. GISH), were unable to do so because their sequences remain too similar. Reprinted by permission of the publisher.

8/3,AB/15 (Item 8 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04761939 H.W. WILSON RECORD NUMBER: BGSA02001939
Hypoviruses and chestnut blight: exploiting viruses to understand and modulate fungal pathogenesis.
Dawe, Angus L
Nuss, Donald L
Annual Review of Genetics v. 35 (2001) p. 1-29
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13672

ABSTRACT: Fungal viruses are considered unconventional because they lack an extracellular route of infection and persistently infect their hosts, often in the absence of apparent symptoms. Because mycoviruses are limited to intracellular modes of transmission, they can be considered as intrinsic fungal genetic elements. Such long-term genetic interactions, even involving apparently asymptomatic mycoviruses, are likely to have an impact on fungal ecology and evolution. One of the clearest examples supporting this view is the phenomenon of hypovirulence (virulence attenuation) observed for strains of the chestnut blight fungus, Cryphonectria parasitica, harboring members of the virus family Hypoviridae. The goal of this chapter is to document recent advances in hypovirus molecular genetics and to provide examples of how that progress is leading to the identification of virus-encoded determinants responsible for altering fungal host phenotype, insights into essential and dispensable elements of hypovirus replication, revelations concerning the role of G-protein signaling in fungal pathogenesis, and new avenues for enhancing biological control potential. Reprinted by permission of the publisher.

8/3,AB/16 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04750973 H.W. WILSON RECORD NUMBER: BGSA02000973
Applied evolution.
Bull, J. J
Wichman, H. A
Annual Review of Ecology and Systematics v. 32 (2001) p. 183-217
SPECIAL FEATURES: bibl graph il tab ISSN: 0066-4162
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 16986

ABSTRACT Evolutionary biology is widely perceived as a discipline with relevance that lies purely in academia. Until recently, that perception was largely true, except for the often neglected role of evolutionary biology in the improvement of agricultural crops and animals. In the past two decades, however, evolutionary biology has assumed a broad relevance extending far outside its original bounds. Phylogenetics, the study of Darwin's theory of "descent with modification," is now the foundation of disease tracking and of the identification of species in medical, pharmacological, or conservation settings. It further underlies bioinformatics approaches to the analysis of genomes. Darwin's "evolution by natural selection" is being used in many contexts, from the design of biotechnology protocols to create new drugs and industrial enzymes, to the avoidance of resistant pests and microbes, to the development of new computer technologies. These examples present opportunities for education of the public and for nontraditional career paths in evolutionary biology. They also provide new research material for people trained in classical approaches. Reprinted by permission of the publisher.

8/3,AB/17 (Item 10 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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14751782 H.W. WILSON RECORD NUMBER: BGSA13000782
The role of breeding system and inbreeding depression in the maintenance of an outcrossing mating strategy in Silene virginica (Caryophyllaceae).
Dudash, Michele R
Fenster, Charles B
American Journal of Botany (Am J Bot) v. 88 no11 (Nov. 2001) p. 1953-9
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7471

ABSTRACT: The goal of this study was to understand the interaction among breeding system, mating system, and expression of inbreeding depression in the hermaphroditic, primarily hummingbird-pollinated, iteroparous, short-lived perennial Silene virginica. We performed hand-selfed and hand-outcrossed pollinations in the field, conducted detailed floral observations within individual flowers and plants, and assayed adult tissue from flowering plants for a genetic estimate of population outcrossing rate. We quantified the opportunity for geitonogamy as the proportion of days each plant exhibited simultaneous male and female function, i.e., asynchronous expression of male- and female-phased flowers. Expression of cumulative inbreeding depression based on germination rate and total flower production in the glasshouse was (similar)40% and was congruent with the estimated high outcrossing rate of 0.89. Floral observations demonstrated strong temporal protandry within each flower (dichogamy) as well as complete spatial separation between male and female function within each flower (herkogamy). On average, 29% of the time there were both male- and female-phased flowers present on an individual plant. We conclude that our estimate of inbreeding depression is compatible with a largely outcrossing mating system and the amount of selfing observed, likely results from geitonogamy. This study illustrates the utility of examining both the causes and the consequences of inbreeding via selfing to provide additional insights into the evolution of plant mating systems. Reprinted by permission of the publisher.

8/3,AB/18 (Item 11 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04669024 H.W. WILSON RECORD NUMBER: BGSA01169024

Traveling toxics: the science, policy, and management of persistent organic pollutants.
Eckley, Noelle
Environment v. 43 no7 (Sept. 2001) p. 24-36
SPECIAL FEATURES: bibl f il map tab ISSN: 0013-9157
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7573

ABSTRACT: International agreements have sought to address the problems caused by the release of persistent organic pollutants (POPs). POPs are organic chemicals characterized by their persistence in the environment, tendency to accumulate in the food chain, and ability to travel long distances in air and water, posing risks to human health and the environment far from the site of their release. Though most countries have banned these chemicals, international action to address POPs does not merely codify the status quo. The signing of the Stockholm Convention, which includes several specific measures to regulate 12 POPs, on May 23, 2001, is a notable example of such action. Indeed, the biggest upcoming policy challenge is the ratification and implementation of the convention; it will enter force only after 50 countries ratify it. Other international activities on chemicals are ongoing, and some address similar substances.

8/3,AB/19 (Item 12 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04657154 H.W. WILSON RECORD NUMBER: BGSA01157154
Wavelet analysis of simulated tropical convective clouds systems. Part II: decomposition of convective-scale and mesoscale structure.
Yang, Jun-Ichi
Moncrieff, Mitchell W; Wu, Xiaoqing
Journal of the Atmospheric Sciences (J Atmos Sci) v. 58 no8 (Apr. 15 2001) p. 868-76
SPECIAL FEATURES: bibl graph il ISSN: 0022-4928
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5207

ABSTRACT: Numerically simulated three-dimensional tropical convective systems were analyzed using a wavelet approach in which the vertical shear of the ambient wind is used as a decomposition criterion. The method objectively decomposes the simulated systems into their two primary components, namely organized deep convection and a mesoscale stratiform region. This reproduces the standard model of highly organized mesoscale convective systems as well as giving an objective characterization of less organized regimes. It demonstrates the vertical component of wind shear as a statistically useful criterion in addition to its better known role as a quasideterministic mechanism controlling the organization of convection and its scale selection. Reprinted by permission of the publisher.

8/3,AB/20 (Item 13 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04519121 H.W. WILSON RECORD NUMBER: BGSA01018121
Transgenic insecticidal corn: the agronomic and ecological rationale for its use.
Ortman, Eldon E
Barry, B. Dean; Buschman, Lawrent L
BioScience (BioScience) v. 51 no11 (Nov. 2001) p. 900-6
SPECIAL FEATURES: bibl ISSN: 0006-3568

LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5700

8/3,AB/21 (Item 14 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04517240 H.W. WILSON RECORD NUMBER: BGSA01017240
FLUXNET: a new tool to study the temporal and spatial variability of ecosystem-scale carbon dioxide, water vapor, and energy flux densities.
Baldocchi, Dennis
Falge, Eva; Gu, Lianhong
Bulletin of the American Meteorological Society (Bull Am Meteorol Soc) v. 82 no11 (Nov. 2001) p. 2415-34
SPECIAL FEATURES: bibl il map ISSN: 0003-0007
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13202

ABSTRACT: FLUXNET is a global network of micrometeorological flux measurement sites that measure the exchanges of carbon dioxide, water vapor, and energy between the biosphere and atmosphere. At present over 140 sites are operating on a long-term and continuous basis. Vegetation under study includes temperate conifer and broadleaved (deciduous and evergreen) forests, tropical and boreal forests, crops, grasslands, chaparral, wetlands, and tundra. Sites exist on five continents and their latitudinal distribution ranges from 70{degree}N to 30{degree}S. FLUXNET has several primary functions. First, it provides infrastructure for compiling, archiving, and distributing carbon, water, and energy flux measurement, and meteorological, plant, and soil data to the science community. (Data and site information are available online at the FLUXNET Web site, http://www-eosdis.ornl.gov/FLUXNET/.) Second, the project supports calibration and flux intercomparison activities. This activity ensures that data from the regional networks are intercomparable. And third, FLUXNET supports the synthesis, discussion, and communication of ideas and data by supporting project scientists, workshops, and visiting scientists. The overarching goal is to provide information for validating computations of net primary productivity, evaporation, and energy absorption that are being generated by sensors mounted on the NASA Terra satellite. Data being compiled by FLUXNET are being used to quantify and compare magnitudes and dynamics of annual ecosystem carbon and water balances, to quantify the response of stand-scale carbon dioxide and water vapor flux densities to controlling biotic and abiotic factors, and to validate a hierarchy of soil-plant-atmosphere trace gas exchange models. Findings so far include 1) net CO2 exchange of temperate broadleaved forests increases by about 5.7 g C m-2 day-1 for each additional day that the growing season is extended; 2) the sensitivity of net ecosystem CO2 exchange to sunlight doubles if the sky is cloudy rather than clear; 3) the spectrum of CO2 flux density exhibits peaks at timescales of days, weeks, and years, and a spectral gap exists at the month timescale; 4) the optimal temperature of net CO2 exchange varies with mean summer temperature; and 5) stand age affects carbon dioxide and water vapor flux densities. Reprinted by permission of the publisher.

8/3,AB/22 (Item 15 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04517138 H.W. WILSON RECORD NUMBER: BGSA01017138
Granule-bound starch synthase (GBSSI) gene phylogeny of wild tomatoes (Solanum L. section Lycopersicon {Mill.} Wettst. subsection

Lycopersicon).
Peralta, Iris E
Spooner, David M
American Journal of Botany (Am J Bot) v. 88 no10 (Oct. 2001) p. 1888-902
SPECIAL FEATURES: bibl il map ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10197

ABSTRACT: Eight wild tomato species are native to western South America and one to the Galapagos Islands. Different classifications of tomatoes have been based on morphological or biological criteria. Our primary goal was to examine the phylogenetic relationships of all nine wild tomato species and closely related outgroups, with a concentration on the most widespread and variable tomato species Solanum peruvianum, using DNA sequences of the structural gene granule-bound starch synthase (GBSSI, or waxy). Results show some concordance with previous morphology-based classifications and new relationships. The ingroup comprised a basal polytomy composed of the self-incompatible green-fruited species S. chilense and the central to southern Peruvian populations of S. peruvianum, S. habrochaites, and S. pennellii. A derived clade contains the northern Peruvian populations of S. peruvianum (also self-incompatible, green-fruited), S. chmielewskii, and S. neorickii (self-compatible, green-fruited), and the self-compatible red- to orange- to yellow-fruited species S. cheesmaniae, S. lycopersicum, and S. pimpinellifolium. Outgroup relationships are largely concordant with prior chloroplast DNA restriction site phylogenies, support S. juglandifolium and S. ochranthum as the closest outgroup to tomatoes with S. lycopersicoides and S. sitiens as basal to these, and support allogamy, self-incompatibility, and green fruits as primitive in the tomato clade.

9/3,AB/23 (Item 16 from file: 98)
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14515431 H.W. WILSON RECORD NUMBER: BGSA01014431
Functional significance of variation in bryophyte canopy structure.
Rice, Steven K
Collins, David; Anderson, Ann M
American Journal of Botany (Am J Bot) v. 88 no9 (Sept. 2001) p. 1568-76
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8968

ABSTRACT: In most bryophytes, the thickness of boundary layers (i.e., unstirred layers) that surrounds plant surfaces governs rates of water loss. Architectural features of canopies that influence boundary layer thickness affect the water balance of bryophytes. Using field samples (9.3 cm diameter cushions) from 12 populations (11 species) of mosses and liverworts, we evaluated the relationship between canopy structure and boundary layer properties. Canopy structure was characterized using a contact surface probe to measure canopy depth along perpendicular transects at spatial scales ranging from 0.3 to 30 mm on 196 points per sample. Semivariance in depth measurements at different spatial scales was used to estimate three architectural properties: surface roughness (Sr), the scale of roughness elements (Sr), and fine scale surface texture, the latter characterized by the fractal dimension (D) of the canopy profile. Boundary layer properties were assessed by evaporation of ethanol from samples in a wind tunnel at wind speeds from 0.6 to 4.2 m s and applied to characterize mass transfer using principles of dynamic similarity (i.e., using dimensionless representations of conductance and flow). In addition,

particle image velocimetry (PIV) was used to visualize and quantify flow over two species. All cushions exhibited the characteristics of turbulent as opposed to laminar boundary layers, and conductance increased with surface roughness. Bryophyte canopies with higher Lr had greater conductances at all wind speeds. Particle image velocimetry analysis verified that roughness elements interacted with flow and caused turbulent eddies to enter canopies, enhancing evaporation. All three morphological features were significantly associated with evaporation. When Lr, Sr, and D were incorporated with a flow parameter into a conductance model using multiple linear regression, the model accounted for 91% of the variation in mass transfer. Reprinted by permission of the publisher.

8/3,AB/24 (Item 17 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04514582 H.W. WILSON RECORD NUMBER: BGSA01014582
The distribution of estuarine and oceanic water masses on the southern shore of O'ahu, Hawai'i: ecological and coastal management implications, and novel methodology.
Ed Parnell, P
Limnology and Oceanography (Limnol Oceanogr) v. 46 no6 (Sept. 2001) p. 1468-86
SPECIAL FEATURES: bibl il map ISSN: 0024-3590
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11054

ABSTRACT: The distribution of estuarine and oceanic water masses along the shelf of Mamala Bay, O'ahu, Hawaii, were determined by use of larval supply and recruitment patterns of benthic invertebrate species, stable C and N isotopic compositions of the suspension-feeding bivalve, Spondylus tenebrosus, turbidity, drifter, and CTD data. The recruitment of different species among estuaries was used to associate larval species with particular estuarine waters. Recruitment patterns of these species along the shelf were then used to infer water-mass distributions along the shelf. The spatial recruitment pattern of an oceanic lepadomorph barnacle, Conchoderma virgatum, was useful to infer shelf areas exposed to oceanic waters. Water-mass distributions inferred from the recruitment distribution of these species concurred with spatial patterns of turbidity and stable C and N isotopic compositions of S. tenebrosus, as well as drifter observations. Water-mass distributions observed in this study also concurred with biological distributional patterns observed in other studies, such as distributions of phytoplankton and zooplankton and the distribution of coral bio-erosion in the Bay. The ecological implications of this work include further evidence of the physical control of recruitment and biological pattern and the possible control of patch dynamics on the scale of kilometers due to significant recruitment variability at this scale. The prevailing distribution of water masses determined in this study also has important implications for the management of watersheds associated with Mamala Bay. Reprinted by permission of the publisher.

8/3,AB/25 (Item 18 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04511678 H.W. WILSON RECORD NUMBER: BGSA01011678
Implications of mating patterns for conservation of the endangered plant Eriogonum ovalifolium var. vineum (Polygonaceae).
Neel, Maile C
Ross Ibarra, Jeffrey; Ellstrand, Norman C

American Journal of Botany (Am J Bot) v. 88 no7 (July 2001) p. 1214-22
SPECIAL FEATURES: bibl il map ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 9139

ABSTRACT: Mating patterns have direct application to conservation because of their influence on structuring genetic diversity within and among populations and on maintaining that diversity over time. We measured population and family outcrossing rates, biparental inbreeding, correlation of outcrossed paternity, and inbreeding coefficients in six populations from throughout the ecological range of the endangered plant Eriogonum ovalifolium var. vineum using naturally pollinated families. The taxon was primarily outcrossed: population outcrossing rates averaged 0.80 (SE 0.03) and family outcrossing rates averaged 0.88 (SE 0.03); neither rate varied among populations. Five population rates were significantly different from 1 while family rates differed from 1 in only one population. We found high correlated outcrossed paternity and evidence for biparental inbreeding in five populations each. As expected from the predominantly outcrossed mating system, levels of diversity were high and inbreeding coefficients among maternal individuals were low (averaging -0.05, SE 0.12). Differences between inbreeding coefficients of progeny (average 0.21, SE 0.06) and mothers indicated selection against homozygous offspring. These results indicate that it is important to maintain large populations to prevent increases in inbreeding and to maintain pollinator communities to facilitate outcrossing. Reprinted by permission of the publisher.

04509718 H.W. WILSON RECORD NUMBER: BGSA01009718
Transition-matrix model of bioturbation and radionuclide diagenesis.
Shull, David H
Limnology and Oceanography (Limnol Oceanogr) v. 46 no4 (June 2001) p. 905-16
SPECIAL FEATURES: bibl il ISSN: 0024-3590
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 9689

ABSTRACT: Bioturbation rates in muddy sediments are thought to be due primarily to the reworking activities of benthic deposit feeders. However, current mathematical models of bioturbation do not explicitly link rates of particle mixing with realistic biological reworking mechanisms. To address this problem, I present a transition-matrix model of bioturbation that quantitatively links the reworking activities of individual organisms and community-level particle-mixing rates. Solutions to the model are presented for two kinds of tracers; particle-reactive radionuclides with a constant input flux and conservative tracers added to the sediment as a pulse. The model was used to predict the vertical profiles of excess 234Th and 210Pb in the field. The model parameters were determined from benthic community-structure data. Model predictions were then compared to measured profiles of these tracers. On the basis of this comparison, I inferred that maldanid polychaetes at the study site were collecting sediment at the sediment-water interface and depositing it at depth. This transport mechanism had a large effect on the predicted tracer profiles. A sensitivity analysis of the model indicated that deposit feeding by the two most abundant species, Mediomastus ambiseta and Nucula annulata, was the most important process determining the burial rate of the tracers. The model results also indicated that the combined effects of deposit feeding and sedimentation were sufficient to determine the vertical distributions of excess 234Th and 210Pb at the study site. Reprinted by permission of the

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04509214 H.W. WILSON RECORD NUMBER: BGSA01009214
Size-dependent sex allocation within flowers of the annual herb Clarkia unguiculata (Onagraceae): ontogenetic and among-plant variation.
Mazer, Susan J
Dawson, Kelly Ann
American Journal of Botany (Am J Bot) v. 88 no5 (May 2001) p. 819-31
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 11248

ABSTRACT: The relative allocation of resources to male and female functions may vary among flowers within and among individual plants for many reasons. Several theoretical models of sex allocation in plants predict a positive correlation between the resource status of a flower or individual and the proportion of reproductive resources allocated to female function. These models assume that, independent of resource status, a negative correlation exists between male and female investment. Focusing on the allocation of resources within flowers, we tested these theoretical predictions and this assumption using the annual Clarkia unguiculata (Onagraceae). We also sought preliminary evidence for a genetic component to these relationships. From 116 greenhouse-cultivated plants representing 30 field-collected maternal families, multiple flowers and fruits per plant were sampled for gamete production, pollen: ovule ratio, seed number, ovule abortion, seed biomass/fruit, mean individual seed mass, and petal area. If sex allocation changes as predicted, then (1) assuming that flowers produced early have access to more resources than those produced later, basal flowers should exhibit a higher absolute and proportional investment in female function than distal flowers and (2) plants of high resource status (large plants) should produce flowers with a higher proportional investment in female function than those of low resource status. Within plants, variation in floral traits conformed to the first prediction. Among plants and families, no significant effects of plant size (dry stem biomass) on intrafloral proportional sex allocation were observed. We detected no evidence for a negative genetic correlation between male and female investment per flower, even when controlling for plant size. Reprinted by permission of the publisher.

8/3,AB/28 (Item 21 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04508278 H.W. WILSON RECORD NUMBER: BGSA01008278
The evolutionary ecology of nut dispersal.
Vander Wall, Stephen B
The Botanical Review (Bot Rev) v. 67 no1 (Jan./Mar. 2001) p. 74-117
SPECIAL FEATURES: bibl tab ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 27955

ABSTRACT: A variety of nut producing plants have mutualistic seed-dispersal interactions with animals (rodents and corvids) that scatter hoard their nuts in the soil. The goals of this **review** are to summarize the widespread horticultural, botanical, and ecological literature pertaining to nut dispersal in Juglans, Carya, Quercus, Fagus,

Castanae, Castanopsis, Lithocarpus, Corylus, Aesculus, and Prunus; to examine the evolutionary histories of these mutualistic interactions; and to identify the traits of nut-bearing plants and nut-dispersing rodents and jays that influence the success of the mutualism. These interactions appear to have originated as early as the Paleocene, about 60 million years ago. Most nuts appear to have evolved from ancestors with wind-dispersed seeds, but the ancestral form of dispersal in almonds (Prunus spp.) was by frugivorous animals that ingested fruit. Nut-producing species have evolved a number of traits that facilitate nut dispersal by certain rodents and corvids while serving to exclude other animals that act as parasites of the mutualism. Nuts are nutritious food sources, often with high levels of lipids or proteins and a caloric value ranging from 5.7 to 153.5 kJ per propagule, 10-1000 times greater than most wind-dispersed seeds. These traits make nuts highly attractive food items for dispersers and nut predators. The course of nut development tends to reduce losses of nuts to insects, microbes, and nondispersing animals, but despite these measures predispersal and postdispersal nut mortality is generally high. Chemical defenses (e.g., tannins) in the cotyledons or the husk surrounding the nut discourage some nut predators. Masting of nuts (periodic, synchronous production of large nut crops) appears to reduce losses to insects and to increase the number of nuts dispersed by animals, and it may increase cross-pollination. Scatter hoarding by rodents and corvids removes nuts from other sources of nut predation, moves nuts away from source trees where density-dependent mortality is high (sometimes to habitats or microhabitats that favor seedling establishment), and buries nuts in the soil (which reduces rates of predation and helps to maintain nut viability). The large nutrient reserves of nuts not only attract animal dispersers but also permit seedlings to establish a large photosynthetic surface or extensive root system, making them especially competitive in low-light environments (e.g., deciduous forest) and semi-arid environments (e.g., dry mountains, Mediterranean climates). The most important postestablishment causes of seedling failure are drought, insufficient light, browsing by vertebrate herbivores, and competition with forbs and grasses. Because of the nutritional qualities of nuts and the synchronous production of large nut crops by a species throughout a region, nut trees can have pervasive impacts on other members of ecological communities. Nut-bearing trees have undergone dramatic changes in distribution during the last 16,000 years, following the glacial retreat from northern North America and Europe, and the current dispersers of nuts (i.e., squirrels, jays, and their relatives) appear to have been responsible for these movements. Reprinted by permission of the publisher.

04506267 H.W. WILSON RECORD NUMBER: BGSA01006267
Patterns of leaf-pathogen infection in the understory of a Mexican rain forest: incidence, spatiotemporal variation, and mechanisms of infection.
Garcia-Guzman, Graciela
Dirzo, Rodolfo
American Journal of Botany (Am J Bot) v. 88 no4 (Apr. 2001) p. 634-45
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7646

ABSTRACT: This study assessed the levels of damage by leaf pathogens and their variability in terms of host species, space (four mature forest sites) and season of the year (dry and rainy), and the mechanisms of infection in the understory of the Los Tuxtlas tropical rain forest. Sixty-five percent of the species surveyed in the dry season (N: 49) and 64.9% of those surveyed in the rainy season (N = 57) were damaged by fungi.

Leaf area damaged per plant, on average, was <1% (range: 0.25-20.52%). There was considerable variation in the degree of infection among species, but not among sites and seasons. The survey showed that 43% of the leaves were damaged by herbivores and pathogens concurrently, 16% showed damage by insect herbivory alone, and only 1.4% of the sampled leaves showed damage by pathogens alone. Pathogenicity assays experimentally confirmed that the predominant mechanism of fungal establishment was wounding, such as that caused by herbivory (or other similar sources), and only rarely did infection occur through direct contact (without wounds). The results revealed the omnipresence of leaf fungal infection, although with low damage per plant, and the importance of herbivorous insects in the facilitation of fungal infection in tropical understory plants. Reprinted by permission of the publisher.

8/3,AB/30 (Item 23 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04506264 H.W. WILSON RECORD NUMBER: BGSA01006264
Effects of virus infection and light environment on population dynamics of Eupatorium makinoi (Asteraceae).
Funayama, Sachiko
Terashima, Ichiro; Yahara, Tetsukazu
American Journal of Botany (Am J Bot) v. 88 no4 (Apr. 2001) p. 616-22
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 4730

ABSTRACT: We studied the effects of virus infection on dynamics of three Eupatorium makinoi populations in contrasting light environments, Gora-dani (a shaded population) and Minou 1 and Minou 2 (open-site populations). Censuses of the plants were taken for 8 yr in Gora-dani and 4 yr in Minou 1 and Minou 2. After the epidemics of virus infection, most plants were virus infected at both sites. The number of plants and the proportion of flowering individuals decreased rapidly and simultaneously in the shaded population in Goradani. By contrast, in the open-site populations of Minou, the proportion of flowering plants decreased first, and then the number of plants decreased gradually. Growth analysis of the plants in the Gora-dani population revealed that stem growth was significantly suppressed by infection and that flowering and survivorship of the infected plants decreased with reducing plant height. Since light availability affected plant growth and thereby flowering and survivorship, the differences in population dynamics between the two field sites could be caused by the differences in light environments. Although populations in open sites may persist for considerable periods after virus epidemics, the individual local populations of E. makinoi would eventually become extinct irrespective of light environments. Reprinted by permission of the publisher.

8/3,AB/31 (Item 24 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04504733 H.W. WILSON RECORD NUMBER: BGSA01004733
Molecular-functional studies of adaptive genetic variation in prokaryotes and eukaryotes.
Watt, Ward B
Dean, Antony M
Annual Review of Genetics v. 34 (2000) p. 593-622
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English

COUNTRY OF PUBLICATION: United States
WORD COUNT: 13410

ABSTRACT: Knowledge of both prokaryotic and eukaryotic organisms is essential to the study of molecular evolution. Their common ancestry mandates that their molecular functions share many aspects of adaptation and constraint, yet their differences in size, ploidy, and structural complexity also give rise to divergent evolutionary options. We explore the interplay of adaptation, constraint, and neutrality in their evolution by the use of genetic variants to probe molecular function in context of molecular structure, metabolic organization, and phenotype-environment interactions. Case studies ranging from bacteria to butterflies, flies, and vertebrates emphasize, among other points: (a) the importance of moving from initial recording of evolutionary pattern variation to studying the processes underlying the patterns, by experiment, reconstructive inference, or both; (b) the complementarity, not conflict, of finding different performance and fitness impacts of natural variants in prokaryotes or eukaryotes, depending on the nature and magnitude of the variants, their locations and roles in pathways, the nature of molecular function affected, and the resulting organismal phenotype-environment interactions leading to selection or its absence; (c) the importance of adaptive functional interaction of different kinds of variants, as in gene expression variants versus variants altering polypeptide properties, or interaction of changes in enzymes' active sites with complementary changes elsewhere that adjust catalytic function in different ways, or coadaptation of different steps' properties in pathways; (d) the power afforded by combining structural and functional analyses of variants with study of the variants' phenotype-environment interactions to understand how molecular changes affect (or fail to affect) adaptive mechanisms "in the wild." Comparative study of prokaryotes and eukaryotes in this multifaceted way promises to deliver both new insights into evolution and a host o Reprinted by permission of the publisher. Reprinted by permission of the publisher.

8/3,AB/32 (Item 25 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04503815 H.W. WILSON RECORD NUMBER: BGSA01003815
Mechanisms of differential pollen donor performance in wild radish, Raphanus sativus (Brassicaceae).
Marshall, Diane L
Diggle, Pamela K
American Journal of Botany (Am J Bot) v. 88 no2 (Feb. 2001) p. 242-57
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13592

ABSTRACT: In order to understand the characters on which sexual selection might oprate in plants, it is critical to assess the mechanisms by which pollen competition and mate choice occur. To address this issue we measured a number of postpollination characters, ranging from pollen germination and pollen tube growth to final seed paternity, in wild radish. Crosses were performed using four pollen donors on a total of 16 maternal plants (four each from four families). Maternal plants were grown under two watering treatments to evaluate the effects of maternal tissue on the process of mating. The four pollen donors differed significantly in number of seeds sired and differed overall in the mating characters measured. However, it was difficult to associate particular mechanistic characters with ability to sire seeds, perhaps because of interactions among pollen donors within styles or among pollen donors and maternal plants. The process of pollen tube growth and fertilization differed substantially among maternal watering treatments, with many early events occurring more quickly in

stressed plants. Seed paternity, however, was somewhat more even among pollen donors used on stressed maternal plants, suggesting that when maternal tissue is more competent, mating is slowed and is more selective. Reprinted by permission of the publisher.

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04502916 H.W. WILSON RECORD NUMBER: BGSA01002916
Trans-Atlantic dispersal and phylogeograph of Cerastium arcticum (Caryophyllaceae) inferred from RAPD and SCAR markers.
Hagen, Aslaug R
Giese, Henriette; Brochmann, Christian
American Journal of Botany (Am J Bot) v. 88 no1 (Jan. 2001) p. 103-12
SPECIAL FEATURES: bibl graph map tab ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8055

ABSTRACT: Cerastium arcticum is an autogamous pioneer species with a distribution limited to the North Atlantic region. It has been suggested that such species must have survived in ice-free refugia on both sides of the Atlantic throughout the last, or even several, of the Pleistocene glaciations, because they lack special adaptations for long-distance dispersal. To address the possibility for recent trans-Atlantic dispersal of C. arcticum, we analyzed random amplified polymorphic DNA (RAPD) and sequence characterized amplified region (SCAR) differentiation among 26 populations of this high-polyploid species. Three SCAR markers were obtained that verified the main patterns identified in the RAPD analysis. Eighty-four multilocus RAPD phenotypes were observed in the 126 plants analyzed, based on 35 polymorphic markers. Multivariate analyses and analyses of molecular variance (AMOVAs) identified two highly divergent groups of populations: one arctic group (western and eastern Greenland, and the archipelagos of Svalbard and Franz Josef Land) and one nonarctic group (southern and northern Norway, and Iceland), indicating that C. arcticum is composed of two lineages with different evolutionary histories. However, there was little geographic structuring within each lineage, in spite of the fact that both lineages are disjunctly distributed across the Atlantic. Occurrence of very similar, in some cases even identical RAPD multilocus phenotypes on both sides of the Atlantic in this autogamous allopolyploid is most probably caused by postglacial dispersal. The present geographic distribution of C. arcticum may thus have been established after trans-Atlantic expansion from two Weichselian refugia, one for each evolutionary lineage. Unexpectedly, the level of intrapopulational variation increased towards the north. This may reflect that interpopulational migration is most extensive in the treeless arctic environment, where the species has a more continuous distribution than in the more southerly areas. Reprinted by permission of the publisher.

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04383994 H.W. WILSON RECORD NUMBER: BGSA00133994
Perspectives on American mathematics.
Hunger Parshall, Karen
Bulletin of the American Mathematical Society (Bull Am Math Soc) v. 37 no4 (Oct. 2000) p. 381-405
SPECIAL FEATURES: bibl ISSN: 0273-0979
LANGUAGE: English
COUNTRY OF PUBLICATION: United States

WORD COUNT: 14902

ABSTRACT: A research-level community of mathematicians developed in the United States in the closing quarter of the nineteenth century. Since that time, American mathematicians have regularly paused to assess the state of their community and to reflect on its mathematical output. This paper analyzes a series of such reflectionsIAmbeginning with Simon Newcomb's thoughts on the state of the exact sciences in America in 1874 and culminating with the 1988 commentaries on the IDdproblems of mathematicsIDD discussed at Princeton's bicentennial celebrations in 1946IAmagainst a backdrop of broader historical trends. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

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04332840 H.W. WILSON RECORD NUMBER: BGSA00132840
An investigation of ice production mechanisms in small cumuliform clouds using a 3D model with explicit microphysics. Part I: model description.
Ovtchinnikov, Mikhail
Fogan, Yefim L
Journal of the Atmospheric Sciences (J Atmos Sci) v. 57 no18 (Sept. 15 2000) p. 2989-3003
SPECIAL FEATURES: bibl il ISSN: 0022-4928
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12019

ABSTRACT: A new cloud model that combines a three-dimensional nonhydrostatic dynamical framework with explicit liquid- and ice-phase microphysics and a detailed treatment of ice nucleation and multiplication processes is presented. The use of 28 size bins to describe each cloud drop and ice particle spectra allows the authors to account for all major microphysical processes. A detailed scavenging model has been implemented to calculate the collection rate of contact ice nuclei by cloud drops. In addition to contact nucleation, the model accounts for deposition, condensation-freezing, and immersion ice nucleation mechanisms, as well as for secondary ice production via rime splintering. The model performance is illustrated by a simulation of a New Mexican cumulus cloud. Combination of high 100-m spatial resolution with a new initialization procedure that promotes development of small eddies results in a cloud with a more realistic distribution of liquid water content compared to simulations initialized by the standard IDdbubbleIDD approach. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

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DIALOG(R)File 98:General Sci Abs/Full-Text
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04381155 H.W. WILSON RECORD NUMBER: BGSA00131155
Biotechnology and our food supply.
Makey, Maureen A
Santerre, Charles R
Nutrition Today (Nutr Today) v. 35 no4 (July/Aug. 2000) p. 120-8
SPECIAL FEATURES: bibl il ISSN: 0029-666X
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6834

ABSTRACT: Biotechnology and its agricultural applications are discussed. The following topics are covered: the definition of biotechnology,

biotechnology techniques, global experience with genetically improved crops, increased world food supplies, reduced need for chemical pesticides, environmentally friendly crops, safety assessment and regulation of food from genetically modified plants, and enhanced nutritional content, quality, and taste in engineered foods.

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04380222 H.W. WILSON RECORD NUMBER: BGSA00130222
Sensitivity of tropical west Pacific oceanic squall lines to tropospheric wind and moisture profiles.
Lucas, Christopher
Zipser, Edward J; Ferrier, Brad S
Journal of the Atmospheric Sciences (J Atmos Sci) v. 57 no15 (Aug. 1 2000) p. 2351-73
SPECIAL FEATURES: bibl il ISSN: 0022-4928
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13564

ABSTRACT: Two-dimensional experiments using the Goddard Cumulus Ensemble model are performed in order to examine the influence of environmental profiles of wind and humidity on the dynamical and microphysical structure of mesoscale convective systems (MCSs) over the tropical oceans. The initial environments used in this study are derived from the results of a cluster analysis of the TOGA COARE sounding data. The model data are analyzed with methods and measurements similar to those used in observational studies. Experiments to test the sensitivity of MCSs to the thermodynamic profile focus on the role of humidity in the free troposphere. In the experiments, a constant amount of relative humidity is added to every level above the boundary layer. As humidity is increased, model storms transition from weak, unsteady systems with little precipitation to strong, upshear-tilted systems with copious rainfall. This behavior is hypothesized to be the result of the entrainment of environmental air into the updraft cores. Experiments to test the sensitivity of MCSs to the kinematic profile focus on the amount of vertical wind shear in the midlevels, between approximately 2 and 10 km. Five kinematic profiles are used. The dynamical and microphysical characteristics of the runs changed dramatically in different shear environments. Shear in the midlevels affects the convective systems by altering the perturbation pressure field. Stronger shear results in a broader and deeper mesolow below the updraft and a more intense dynamic high above the leading edge. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

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04163252 H.W. WILSON RECORD NUMBER: BGSA00115352
Court in the act.
Mendelson, Joseph
The Ecologist v. 30 no3 (May 2000) p. 48-9
ISSN: 0261-3131
LANGUAGE: English
COUNTRY OF PUBLICATION: United Kingdom
WORD COUNT: 2142

ABSTRACT: The Center for Food Safety has filed a lawsuit against the FDA over its premarket safety-testing and labeling policy on genetically

modified (GM) food. The legal action, filed in the U.S. District Court of Columbia on May 27, 1998, was taken in response to the FDA's deregulation of genetically engineered foods in 1992 on the basis that GM foods present no different risks than do traditional foods. The Center for Food Safety lawsuit seeks to mandate the FDA to treat all genetic modifications to food produced by genetic engineering methods as food additives, to carry out a comprehensive environmental **review** of all GM foods made commercially available, and to ensure the labeling of all GM foods.

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04273994 H.W. WILSON RECORD NUMBER: BGSA00023994
Interim report on genomics of Escherichia coli.
Riley, M
Serres, M. H
Annual Review of Microbiology v. 54 (2000) p. 341-411
SPECIAL FEATURES: bibl tab ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 25680

ABSTRACT: We present a summary of recent progress in understanding Escherichia coli K-12 gene and protein functions. New information has come both from classical biological experimentation and from using the analytical tools of functional genomics. The content of the E. coli genome can clearly be seen to contain elements acquired by horizontal transfer. Nevertheless, there is probably a large, stable core of >3500 genes that are shared among all E. coli strains. The gene-enzyme relationship is examined, and, in many cases, it exhibits complexity beyond a simple one-to-one relationship. Also, the E. coli genome can now be seen to contain many multiple enzymes that carry out the same or closely similar reactions. Some are similar in sequence and may share common ancestry; some are not. We discuss the concept of a minimal genome as being variable among organisms and obligatorily linked to their life styles and defined environmental conditions. We also address classification of functions of gene products and avenues of insight into the history of protein evolution. Reprinted by permission of the publisher.

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DIALOG(R)File 98:General Sci Abs/Full-Text
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04272907 H.W. WILSON RECORD NUMBER: BGSA00022907
Mercury toxicity in plants.
Patra, Manomita
Sharma, Anchana
The Botanical Review (Bot Rev) v. 66 no3 (July/Sept. 2000) p. 379-422
SPECIAL FEATURES: bibl il tab ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 25426

ABSTRACT: Mercury poisoning has become a problem of current interest as a result of environmental pollution on a global scale. Natural emissions of mercury form two-thirds of the input; manmade releases form about one third. Considerable amounts of mercury may be added to agricultural land with sludge, fertilizers, lime, and manures. The most important sources of contaminating agricultural soil have been the use of organic mercurials as a seed-coat dressing to prevent fungal diseases in seeds. In general, the effect of treatment on germination is favorable when

recommended dosages are used. Injury to the seed increases in direct proportion to increasing rates of application. The availability of soil mercury to plants is low, and there is a tendency for mercury to accumulate in roots, indicating that the roots serve as a barrier to mercury uptake. Mercury concentration in aboveground parts of plants appears to depend largely on foliar uptake of Hg0 volatilized from the soil. Uptake of mercury has been found to be plant specific in bryophytes, lichens, wetland plants, woody plants, and crop plants. Factors affecting plant uptake include soil or sediment organic content, carbon exchange capacity, oxide and carbonate content, redox potential, formulation used, and total metal content. In general, mercury uptake in plants could be related to pollution level. With lower levels of mercury pollution, the amounts in crops are below the permissible levels. Aquatic plants have shown to be bioaccumulators of mercury. Mercury concentrations in the plants (stems and leaves) are always greater when the metal is introduced in organic form. In freshwater aquatic vascular plants, differences in uptake rate depend on the species of plant, seasonal growth-rate changes, and the metal ion being absorbed. Some of the mercury emitted from the source into the atmosphere is absorbed by plant leaves and migrates to humus through fallen leaves. Mercury-vapor uptake by leaves of the C3 species oats, **barley**, and **wheat** is five times greater than that by leaves of the C4 species corn, sorghum, and crabgrass. Such differential uptake by C3 and C4 species is largely attributable to internal resistance to mercury-vapor binding. Airborne mercury thus seems to contribute significantly to the mercury content of crops and thereby to its intake by humans as food. Accumulation, toxicity response, and mercury distribution differ between plants exposed through shoots or through roots, even when internal mercury concentrations in the treated plants are similar. Throughfall and litterfall play a significant role in the cycling and deposition of mercury. The possible causal mechanisms of mercury toxicity are changes in the permeability of the cell membrane, reactions of sulphydryl (-SH) groups with cations, affinity for reacting with phosphate groups and active groups of ADP or ATP, and replacement of essential ions, mainly major cations. In general, inorganic forms are thought to be more available to plants than are organic ones. Reprinted by permission of the publisher.

04272503 H.W. WILSON RECORD NUMBER: BGSA00022503
Synthesis of native proteins by chemical ligation.
Dawson, Philip E
Kent, Stephen B. H
Annual Review of Biochemistry v. 69 (2000) p. 923-60
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12238

ABSTRACT: In just a few short years, the chemical ligation of unprotected peptide segments in aqueous solution has established itself as the most practical method for the total synthesis of native proteins. A wide range of proteins has been prepared. These synthetic molecules have led to the elucidation of gene function, to the discovery of novel biology, and to the determination of new three-dimensional protein structures by both NMR and X-ray crystallography. The facile access to novel analogs provided by chemical protein synthesis has led to original insights into the molecular basis of protein function in a number of systems. Chemical protein synthesis has also enabled the systematic development of proteins with enhanced potency and specificity as candidate therapeutic agents. Reprinted by permission of the publisher.

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04272490 H.W. WILSON RECORD NUMBER: BGSA00022490
Protein splicing and related forms of protein autoprocessing.
Paulus, Henry
Annual Review of Biochemistry v. 69 (2000) p. 447-96
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 18571

ABSTRACT: Protein splicing is a form of posttranslational processing that consists of the excision of an intervening polypeptide sequence, the intein, from a protein, accompanied by the concomitant joining of the flanking polypeptide sequences, the exteins, by a peptide bond. It requires neither cofactors nor auxiliary enzymes and involves a series of four intramolecular reactions, the first three of which occur at a single catalytic center of the intein. Protein splicing can be modulated by mutation and converted to highly specific self-cleavage and protein ligation reactions that are useful protein engineering tools. Some of the reactions characteristic of protein splicing also occur in other forms of protein autoprocessing, ranging from peptide bond cleavage to conjugation with nonprotein moieties. These mechanistic similarities may be the result of convergent evolution, but in at least one case--hedgehog protein autoprocessing--there is definitely a close evolutionary relationship to protein splicing. Reprinted by permission of the publisher.

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04267707 H.W. WILSON RECORD NUMBER: BGSA00017707
Factors affecting establishment of a gypsophyte: the case of Lepidium subulatum (Brassicaceae).
Escudero, Adrian
Iriondo, Jose M; Olano, Jose M
American Journal of Botany (Am J Bot) v. 87 no6 (June 2000) p. 861-71
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10321

ABSTRACT: The restriction of vascular plants to gypsum-rich soils under arid or semiarid climates has been reported by many authors in different parts of the world. However, factors controlling the presence of gypsophytes on these soils are far from understood. We investigated the establishment of Lepidium subulatum, a gypsophyte, in a nondisturbed semiarid gypsum-soil landscape in central Spain, both from spatial and temporal perspectives. Over 1400 seedlings were tagged, and their growth and survival were monitored for a 2-yr period. Several biotic and abiotic variables were measured to determine the factors controlling the emergence and early survival. These variables included the cover of annual plants, bryophytes, lichens, litter, gypsum crystals, bare fraction and cover of each perennial plant, and several soil properties (gravel, fine gravel, and fine-earth fraction, conductivity, pH, gypsum content, organic matter and penetrometer soil resistance). Our results support the linkage of gypsophily with some physical properties of the surface crust. Seedlings tended to establish on the gypsum surface crust, and their survival was size dependent, probably as a consequence of the necessity of rooting below the surface crust before summer drought arrives. However, once seedlings

emerged, a higher survival rate occurred on the alluvial soils of the piedmont-slope boundary where soil crusts are absent or thinner. We conclude that Lepidium subulatum may be considered a refuge model endemic with a distribution range that occupies a reduced fraction of a wider habitat from which it is probably excluded by competition. Reprinted by permission of the publisher.

8/3,AB/44 (Item 37 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04165194 H.W. WILSON RECORD NUMBER: BGSA00015194
LEAFY and the evolution of rosette flowering in violet cress (Jonopsidium acaule, Brassicaceae).
Shu, Guoping
Amaral, Weber; Hileman, Lena C
American Journal of Botany v. 87 no5 (May 2000) p. 634-41
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5493

ABSTRACT: Arabidopsis and most other Brassicaceae produce an elongated inflorescence of mainly ebracteate flowers. However, the early-flowering species violet cress (Jonopsidium acaule) and a handful of other species produce flowers singly in the axils of rosette leaves. In Arabidopsis the gene LEAFY (LFY) is implicated in both the determination of flower meristem identity and in the suppression of leaves (bracts) that would other wise subtend the flowers. In this study we examined the role of LFY homologs in the evolution of rosette flowering in violet cress. We cloned two LFY homologs, vcLFY1 and vcLFY2, from violet cress. Their exon sequences show 90% nucleotide similarity with Arabidopsis LFY and 99% similarity to each other. We used in situ hybridization to study vcLFY expression in violet cress. The patterns were very similar to LFY in Arabidopsis except for stronger expression in the shoot apical meristem outside of the region of flower meristem initiation. It is possible that the relatively diffuse expression of vcLFY contributes to the lack of bract suppression in violet cress. Additionally, the earliest flowers produced by violet cress express vcLFY, suggesting that accelerated flowering in violet cress could also result from changes in the regulation of vcLFY. Reprinted by permission of the publisher.

8/3,AB/45 (Item 38 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04164504 H.W. WILSON RECORD NUMBER: BGSA00014504
Crown gall disease and Agrobacterium tumefaciens: a study of the history, present knowledge, missing information, and impact on molecular genetics.
Stafford, Helen A
The Botanical Review (Bot Rev) v. 66 no1 (Jan./Mar. 2000) p. 99-118
SPECIAL FEATURES: bibl il ISSN: 0006-8101
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10929

ABSTRACT: The production of crown gall tumors in plants caused by Agrobacterium tumefaciens represents a unique disease involving the transfer of DNA from the bacterium to the nucleus of the plant. Vital aspects of this transfer are still being studied. Reprinted by permission of the publisher.

8/3,AB/46 (Item 39 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04264428 H.W. WILSON RECORD NUMBER: BGSA00014428
Phylogeny of the Bangiophycidae (Rhodophyta) and the secondary endosymbiotic origin of algal plastids.
Oliveira, Mariana C
Bhattacharya, Debashish
American Journal of Botany (Am J Bot) v. 87 no4 (Apr. 2000) p. 482-92
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8143

ABSTRACT: The Rhodophyta (red algae) are composed of the subclasses Bangiophycidae and Florideophycidae. Two evolutionarily interesting features of the Bangiophycidae are: (1) they are the ancestral pool from which the more morphologically complex taxa in the Florideophycidae have arisen and (2) they are the sources of the plastids, through secondary endosymbioses, for the Cryptophyta, Haptophyta, and the Heterokonta. To understand Bangiophycidae phylogeny and to gain further insights into red algal secondary endosymbioses, we sequenced the plastid-encoded small subunit ribosomal DNA (rDNA) coding region from nine members of this subclass and from two members of the Florideophycidae. These sequences were included in phylogenetic analyses with all available red algal plus chlorophyll a + c algal plastid rDNA coding regions. Our results are consistent with a monophyletic origin of the Florideophycidae with these taxa forming a sister group of the Bangiales. The Bangiophycidae is of a paraphyletic origin with orders such as the Porphyridiales polyphyletic and distributed over three independent red algal lineages. The plastids of the heterokonts are most closely related to members of the Cyanidium--Galdieria group of Porphyridiales and are not directly related to cryptophyte and haptophyte plastids. The phylogenies provide strong evidence for the independent origins of these "complex" algal plastids from different members of the Bangiophycidae. Reprinted by permission of the publisher.

8/3,AB/47 (Item 40 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04259241 H.W. WILSON RECORD NUMBER: BGSA00009241
Gene mapping in the 20th and 21st centuries: statistical methods, data analysis, and experimental design.
Terwilliger, Joseph D
Goring, Harald H. H
Human Biology (Hum Biol) v. 72 no1 (Feb. 2000) p. 63-132
SPECIAL FEATURES: bibl il ISSN: 0018-7143
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 31712

ABSTRACT: Part of a special section on anthropological genetics in the 21st century. The theory and practice of gene mapping at the end of the 20th century are **reviewed**. Most methods of linkage and linkage disequilibrium analysis are shown to be similar fundamentally, with differences between them being related more to study design and ascertainment than to technical details of the underlying statistical analysis. A new focus in the field of statistical genetics is proposed that highlights more clearly the primacy of study design as the means to increase power for gene mapping.

8/3,AB 48 (Item 41 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04256372 H.W. WILSON RECORD NUMBER: BGSA00006372
Perspective: the pace of modern life: measuring rates of contemporary microevolution.
Hendry, Andrew P
Kinnison, Michael T
Evolution (Evolution) v. 53 no6 (Dec. 1999) p. 1637-53
SPECIAL FEATURES: bibl il ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 14481

ABSTRACT: We evaluate methods for measuring and specifying rates of microevolution in the wild, with particular regard to studies of contemporary, often deemed "rapid," evolution. A considerable amount of ambiguity and inconsistency persists within the field, and we provide a number of suggestions that should improve study design, inference, and clarity of presentation. (1) Some studies measure change over time within a population (allochronic) and others measure the difference between two populations that had a common ancestor in the past (synchronic). Allochronic studies can be used to estimate rates of "evolution," whereas synchronic studies more appropriately estimate rates of "divergence." Rates of divergence may range from a small fraction to many times the actual evolutionary rates in the component populations. (2) Some studies measure change using individuals captured from the wild, whereas others measure differences after rearing in a common environment. The first type of study can be used to specify "phenotypic" rates and the later "genetic" rates. (3) The most commonly used evolutionary rate metric, the darwin, has a number of theoretical shortcomings. Studies of microevolution would benefit from specifying rates in standard deviations per generation, the haldane. (4) Evolutionary rates are typically specified without an indication of their precision. Readily available methods for specifying confidence intervals and statistical significance (regression, bootstrapping, randomization) should be implemented. (5) Microevolutionists should strive to accumulate time series, which can reveal temporal shifts in the rate of evolution and can be used to identify evolutionary patterns. (6) Evolutionary rates provide a convenient way to compare the tempo of evolution across studies, traits, taxa, and time scales, but such comparisons are subject to varying degrees of confidence. Comparisons across different time scales are particularly tenuous. (7) A number of multivariate rate measures exist, but considerable theoretical development is required before their utility can be determined. We encourage the continued investigation of evolutionary rates because the information they provide is relevant to a wide range of theoretical and practical issues.

8/3,AB 49 (Item 42 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04255640 H.W. WILSON RECORD NUMBER: BGSA00005640
Plant retrotransposons.
AUGMENTED TITLE: **review**
Kumar, Amar
Bennetzen, Jeffrey L
Annual Review of Genetics v. 33 (1999) p. 479-532
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States

COUNTRY OF PUBLICATION: United States
WORD COUNT: 8359

ABSTRACT: Phylogenetic analyses of partial phytochrome B (PHYB) nuclear DNA sequences provide unambiguous resolution of evolutionary relationships within Poaceae. Analysis of PHYB nucleotides from 51 taxa representing seven traditionally recognized subfamilies clearly distinguishes three early diverging herbaceous "bambusoid" lineages. First and most basal are Anomochloa and Streptochaeta, second is Pharus, and third is Puelia. The remaining grasses occur in two principal, highly supported clades. The first comprises bambusoid, oryzoid, and pooid genera (the BOP clade); the second comprises panicoid, arundinoid, chloridoid, and centothecoid genera (the PACC clade). The PHYB phylogeny is the first nuclear gene tree to address comprehensively phylogenetic relationsnips among grasses. It corroborates several inferences made from chloroplast gene trees, including the PACC clade, and the basal position of the herbaceous bamboos Anomochloa, Streptochaeta, and Pharus. However, the clear resolution of the sister group relationship among bambusoids, oryzoids, and pooids in the PHYB tree is novel: the relationship is only weakly supported in ndhF trees and is nonexistent in rbcL and plastid restriction site trees. Nuclear PHYB data support Anomochlooideae, PHaroideae, Pooideae sensu lato, Oryzoideae, Panicoideae, and Chloridoideae, and concur in the polyphyly of both Arundinoideae and Bambusoideae. Reprinted by permission of the publisher.

8/3,AB/52 (Item 45 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04050531 H.W. WILSON RECORD NUMBER: BGSA99050531
Chloroplast DNA evidence for the evolution of Microseris (Asteraceae) in Australia and New Zealand after long-distance dispersal from western North America.
Vijverberg, Kitty
Mes, Ted H. M; Bachmann, Konrad
American Journal of Botany v. 86 no10 (Oct. 1999) p. 1448-63
SPECIAL FEATURES: bibl il map ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10164

ABSTRACT: Restriction site mutations and trnL(UAA)-trnF(GAA) intergenic spacer length variants in the chloroplast genome were used to investigate the phylogenetic relationships among 53 Australian and New Zealand Microseris populations and to assess their position within their primarily North American genus. The study was performed to enhance understanding of evolutionary processes within this unique example of intercontinental dispersal and subsequent adaptive radiation. A southern blot method using four-base restriction enzymes and fragment separation on polyacryamide gels resulted in 55 mutations of which 30 were potentially phylogenetically informative. Most mutations were small indels of <162 bp, 80% of which were <21 bp. The small indels were useful for phylogenetic reconstruction of Australasian Microseris as judged by the high consistency indexes. The results confirmed the monophyly of the Australian and New Zealand Microseris. The occurrence of "hard" basal polytomies in the most parsimonious trees indicated that rapid radiation has occurred early in the history of the taxon. The monophyly of M. lanceolata, which includes the self-incompatible ecotypes of the Australian mainland, was confirmed. Within this species three clades were found that reflect more geographic distribution than morphological entities, suggesting that migration and possibly introgression between different ecotypes, or parallel evolution of similar adaptations, has occurred. One of the three clades was supported by a 162-bp deletion in the trnL-trnF spacer, while a subgroup of this exhibited also a tandemly repeated trnF exon. The data were inconclusive

about the monophyly of the second Australasian species, M. scapigera, which comprises the New Zealand, Tasmanian, and autofertile ecotypes of Australia. Reprinted by permission of the publisher.

8/3,AB/53 (Item 46 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04050513 H.W. WILSON RECORD NUMBER: BGSA99050513
Bacterial biocatalysts: molecular biology, three-dimensional structures, and biotechnological applications of lipases.
AUGMENTED TITLE: **review**
Jaeger, K-E
Dijkstra, B. W; Reetz, M. T
Annual Review of Microbiology v. 53 (1999) p. 315-51
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 14938

ABSTRACT: Bacteria produce and secrete lipases, which can catalyze both the hydrolysis and the synthesis of long-chain acylglycerols. These reactions usually proceed with high regioselectivity and enantioselectivity, and, therefore, lipases have become very important stereoselective biocatalysts used in organic chemistry. High-level production of these biocatalysts requires the understanding of the mechanisms underlying gene expression, folding, and secretion. Transcription of lipase genes may be regulated by quorum sensing and two-component systems; secretion can proceed either via the Sec-dependent general secretory pathway or via ABC transporters. In addition, some lipases need folding catalysts such as the lipase-specific foldases and disulfide-bond--forming proteins to achieve a secretion-competent conformation. Three-dimensional structures of bacterial lipases were solved to understand the catalytic mechanism of lipase reactions. Structural characteristics include an a/b hydrolase fold, a catalytic triad consisting of a nucleophilic serine located in a highly conserved Gly-X-Ser-X-Gly pentapeptide, and an aspartate or glutamate residue that is hydrogen bonded to a histidine. Four substrate binding pockets were identified for triglycerides: an oxyanion hole and three pockets accommodating the fatty acids bound at positions sn-1, sn-2, and sn-3. The differences in size and the hydrophilicity/hydrophobicity of these pockets determine the enantiopreference of a lipase. The understanding of structure-function relationships will enable researchers to tailor new lipases for biotechnological applications. At the same time, directed evolution in combination with appropriate screening systems will be used extensively as a novel approach to develop lipases with high stability and enantioselectivity. Reprinted by permission of the publisher.

8/3,AB/54 (Item 47 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04045904 H.W. WILSON RECORD NUMBER: BGSI99045904
Cellular and molecular biology of the aquaporin water channels.
Borgnia, Mario
Nielsen, S ren; Engel, Andreas
Annual Review of Biochemistry v. 68 (1999) p. 425-58
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12474

ABSTRACT: The high water permeability characteristic of mammalian red cell membranes is now known to be caused by the protein AQP1. This channel freely permits movement of water across the cell membrane, but it is not permeated by other small, uncharged molecules or charged solutes. AQP1 is a tetramer with each subunit containing an aqueous pore likened to an hourglass formed by obversely arranged tandem repeats. Cryoelectron microscopy of reconstituted AQP1 membrane crystals has revealed the three-dimensional structure at 3-6 A. AQP1 is distributed in apical and basolateral membranes of renal proximal tubules and descending thin limbs as well as capillary endothelia. Ten mammalian aquaporins have been identified in water-permeable tissues and fall into two groupings. Orthodox aquaporins are water-selective and include AQP2, a vasopressin-regulated water channel in renal collecting duct, in addition to AQP0, AQP4, and AQP5. Multifunctional aquaglyceroporins AQP3, AQP7, and AQP9 are permeated by water, glycerol, and some other solutes. Aquaporins are being defined in numerous other species including amphibia, insects, plants, and microbials. Members of the aquaporin family are implicated in numerous physiological processes as well as the pathophysiology of a wide range of clinical disorders. Reprinted by permission of the publisher.

8/3,AB/55 (Item 48 from file: 98)
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04042080 H.W. WILSON RECORD NUMBER: BGSA99042080
Genetic relationships between parasite virulence and transmission in the rodent malaria Plasmodium chabaudi.
Mackinnon, Margaret J
Read, Andrew F
Evolution (Evolution) v. 53 no3 (June 1999) p. 689-703
SPECIAL FEATURES: bibl il ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10646

ABSTRACT: Genetic relationships between virulence and transmission in the rodent malarial parasite Plasmodium chabaudi were investigated. Two assumptions of the parasite-centered trade-off model of the evolution of virulence--that higher replication rates lead to higher levels of virulence and to higher levels of transmission--were tested using inbred laboratory mice infected with P. chabaudi. The virulence and transmission of 8 parasite clones isolated from the wild were measured, and the across-clone genetic relationships between replication rate, virulence, and transmission were examined. Results supported the validity of both assumptions.

8/3,AB/56 (Item 49 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04038175 H.W. WILSON RECORD NUMBER: BGSI99038175
Blood pressure: genetic and environmental influences.
Gerber, Linda M
Halberstein, Robert A
Human Biology (Hum Biol) v. 71 no4 (Aug. 1999) p. 467-73
SPECIAL FEATURES: bibl il ISSN: 0018-7143
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 106936

ABSTRACT: An introduction to a special issue on blood pressure and its genetic and environmental influences. Some of the specific aspects related to blood pressure variation are addressed in this issue. The aim of the

issue is to help bring together a vast and ever growing body of research and reveal areas for future research. The history of blood pressure research is outlined, and a brief description of each of the 9 papers in the issue is given.

8/3,AB/57 (Item 50 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04036555 H.W. WILSON RECORD NUMBER: BGSA99036555
Wind pollination and reproductive assurance in Linanthus parviflorus (Polemoniaceae), a self-incompatible annual.
Goodwillie, Carol
American Journal of Botany (Am J Bot) v. 86 no7 (July 1999) p. 948-54
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6437

ABSTRACT: Wind pollination was experimentally demonstrated in Linanthus parviflorus (Polemoniaceae), a predominantly beefly-pollinated, self-incompatible annual. Seed set in plants enclosed in mesh tents that excluded pollinators but allowed airborne pollen flow provided evidence for wind pollination, and the extent of seed set due to wind pollination was compared to that in open-pollinated controls and pollen-supplemented treatments. Additional controls were included to test for possible confounding effects of the mesh tent. Mean seed number in open-pollinated plants was 72.8-81.1% of that in pollen-supplemented plants, while wind pollination alone produced 49.5-51.2%, a smaller but substantial proportion of seed set with pollen supplementation. Further evidence for wind pollination was found in a comparison of sites differing in the extent of wind exposure in two populations of L. parviflorus. Airborne pollen counts were higher in exposed sites than in protected sites, and the difference was marginally significant. Seed set was significantly pollen limited in protected sites, but not in exposed sites. Taken together, the data suggest that wind pollination provides some reproductive assurance in this obligately outcrossing species. Wind pollination is hypothesized to represent an alternative to selfing as an evolutionary solution to the problem of temporal or spatial variation in pollination visitation. Reprinted by permission of the publisher.

8/3,AB/58 (Item 51 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04027979 H.W. WILSON RECORD NUMBER: BGSA99027879
Geographic distribution of molecular variance within the blue marlin (Makaira nigricans): a hierarchical analysis of allozyme, single-copy nuclear DNA, and mitochondrial DNA markers.
Buonaccorsi, Vincent P
Reece, Kimberly S; Morgan, Lee W
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 563-79
SPECIAL FEATURES: bibl il map ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 9653

ABSTRACT: A comparative hierarchical analysis of variance applied to 3 classes of molecular markers within the blue marlin (Makaira nigricans) is described. Four polymorphic allozyme loci, 4 polymorphic anonymously chosen single copy nuclear DNA (scnDNA) loci, and previously reported restriction fragment length polymorphisms (RFLPs) of mitochondrial DNA (mtDNA) were

included in the study. Moderate levels of genetic variation were detected at both polymorphic allozyme and scnDNA loci. However, mtDNA markers showed much greater diversity. At 3 of 4 allozyme loci and 3 of 4 scnDNA loci, allele frequencies were significantly different between Atlantic and Pacific Ocean samples. Compared with divergence detected at nuclear loci, mtDNA RFLP divergence between oceans was significantly greater. The difference observed between nuclear and mitochondrial divergence estimates may be due to the 4-fold smaller effective population size of mtDNA and male-mediated gene flow

8/3,AB/59 (Item 52 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04027636 H.W. WILSON RECORD NUMBER: BGSA99027636
Integrating developmental evolutionary patterns and mechanisms: a case study using the gastropod radula.
Buralnick, R. P
Lindberg, D. R
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 447-59
SPECIAL FEATURES: bibl il ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10416

ABSTRACT: The patterns and processes of shape change in a model system, the gastropod radula, were examined. The gastropod radula possesses a simple system, having only 2 processes, initial selection and postsecretional movement of teeth. Taken together, the results of this study showed that 2 different ontogenetic processes can lead to similar expression of row shapes; therefore, phylogenetic homologies based on adult morphologies and ontogenetic process may be discordant.

8/3,AB/60 (Item 53 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04027633 H.W. WILSON RECORD NUMBER: BGSA99027633
Dynamic and genetic consequences of variation in horizontal transmission for a microparasitic infection.
Schmid-Hempel, Paul
Fuhr, Katina; Kruger, Nadja
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 426-34
SPECIAL FEATURES: bibl il ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 7555

ABSTRACT: The way in which variation in the time to transmission and exposure to adverse conditions outside the host interact to determine the success of the infection in the next host was investigated using the trypanosome Crithidia bombi infecting its bumblebee host (Bombus terrestris). Overall, the findings show that the window of transmission was comparably less important than the transmission mode. Low host densities were seen to decrease the rate of contacts with new hosts and to decrease success because parasites had to wait longer at a transmission site.

8/3,AB/61 (Item 54 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04022237 H.W. WILSON RECORD NUMBER: BGSA99022237
Most unwanted: persistent organic pollutants.
Fisher, Brandy E
Environmental Health Perspectives (Environ Health Perspect) v. 107 no1 (Jan. 1999) p. A18-A23
SPECIAL FEATURES: il ISSN: 0091-6765
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 5434

ABSTRACT: A dozen chemicals have been identified by the UN Environmental Programme as powerful threats to human and wildlife health on a global basis. These chemicals belong to a class known as persistent organic pollutants, which are chemicals that can travel thousands of miles, accumulate in the food chain, and persist in the environment, taking up to centuries to fully degrade. Such compounds have been known to cause birth defects, various cancers, immune system dysfunction, and reproductive problems in wildlife. The 12 compounds are aldrin, chlordane, DDT, dieldrin, dioxins, endrin, furans, heptachlor, hexachlorobenzene, mirex, polychlorinated biphenyls, and toxaphene. The properties of these compounds, and some alternatives to them, are discussed.

8/3,AB/62 (Item 55 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04014874 H.W. WILSON RECORD NUMBER: BGSI99014874
The influence of population size and isolation on gene flow by pollen in Silene alba.
Richards, Christopher M
Church, Sheri; McCauley, David E
Evolution (Evolution) v. 53 no1 (Feb. 1999) p. 63-73
SPECIAL FEATURES: bibl il ISSN: 0014-3820
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8643

ABSTRACT: The effects of flower number and distance between patches on gene flow by pollen in Silene alba were investigated. At 20 m, the mean immigration rate was just over 47 percent, whereas immigration rates were less than 6 percent at 80 m. The number of flowers in the focal and neighboring populations had a significant effect on the frequency of gene flow. Factors that influenced gene flow at one spatial scale did not act in the same way at another. The patterns of gene flow within a metapopulation system can be complex and may vary within a growing season.

8/3,AB/63 (Item 56 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04014401 H.W. WILSON RECORD NUMBER: BGSI99014401
Heat-shock proteins, molecular chaperones, and the stress response: evolutionary and ecological physiology.
AUGMENTED TITLE: **review**
Feder, Martin E
Hofmann, Gretchen E
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82
SPECIAL FEATURES: bibl il ISSN: 0066-4278
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual **Review** of Physiology, Volume 61, 1999, by Annual **Reviews** Inc. (http://www.annurev.org).

8/3,AB/64 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
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0269200 DBA Accession No.: 2001-08482
Strategies for expressing multiple foreign genes in plants as polycistronic constructs - **vector**-mediated multiple transgene gene transfer and expression in transgenic plant for crop improvement, antibody, polymer or beta-carotene preparation; a **review**
AUTHOR: Hunt A G; Maiti I B
CORPORATE AFFILIATE: Univ.Kentucky Univ.Kentucky-Tobacco-Health-Res.Inst.
CORPORATE SOURCE: Department of Agronomy, N212A Agriculture Science Center North, 500 South Limestone Street, Lexington, KY 40546-0091, USA. email:aghunt00@pop.uky.edu
JOURNAL: In Vitro Cell.Dev.Biol.Plant (37, 3, 313-20) **2001**
ISSN: 1054-5476 CODEN: IVCPEO
LANGUAGE: English
ABSTRACT: Strategies for expressing multiple foreign genes in plants as polycistronic constructs are **reviewed**. There is an increased desire to express many foreign genes in the same transgenic plant. A range of approaches have been explored in the period since gene transfer was developed as a useful tool in plant science. These approaches have ranged from assembly of multiple transcription units on a single DNA **vector**, to the execution of several independent **transformations** involving single genes followed by successive rounds of hybridization to yield plant lines with the desired combination of genes, to cotransformation with multiple plasmids followed by molecular screening to identify desired transgenic plants. Recent developments have provided new alternatives to the problem of the expression of multiple transgenes in plants, approaches that are based on the expression of polycistronic mRNAs. Among the more exciting advances in recent years has been the use of multigene expression to produce transgenic plants capable of synthesizing antibodies, biodegradable polymers, and beta-carotenes in **rice** (Oryza sativa) endosperms. (54 ref)

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DIALOG(R)File 357:Derwent Biotech Res.
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0262697 DBA Accession No.: 2001-02273
Production of agronomically superior transgenic **rice** plants using Agrobacterium **transformation** methods: present status and future perspectives - Agrobacterium tumefaciens-mediated gene transfer and expression in **rice** transgenic plant for crop improvement; a **review**
AUTHOR: Roy M; +Jain R K; Rohila J S; Wu R
CORPORATE AFFILIATE: Univ.Cornell Bose-Inst.Calcutta Univ.Haryana-Agr.
CORPORATE SOURCE: Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar 125 004, India.
email:rkjain@hau.hry.nic.in
JOURNAL: Curr.Sci. (79, 7, 954-60) **2000**
ISSN: 0011-3891 CODEN: CUSCAM
LANGUAGE: English
ABSTRACT: The production of agronomically superior transgenic **rice** (Oryza sativa) plants using Agrobacterium sp. **transformation** methods and their present status and future perspectives are **reviewed**. Agrobacterium tumefaciens is a soil bacterium that can genetically **transform** plant cells by transferring defined piece of DNA (known as T-DNA) from its tumor-inducing (Ti) plasmid into the genome of infected plants. A large number of suitable **vectors** have been developed for Agrobacterium sp.-mediated **transformation** . This method also provides an opportunity to transfer large segments of DNA that may contain more than 10 genes without rearrangement, which are suitable for studying their cumulative, interactive effects on complex polygenic traits. This transfer method has given results of high-efficiency of Agrobacterium-mediated production of fertile and heritable transgenic **rice** plants. This technology has been adopted by many laboratories and is now in wide-spread use. This method of **transformation** has several advantages, including higher **transformation** efficiency, integration of relatively low number of transgene copies and low experimental costs. (76 ref)

8/3,AB/66 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0242811 DBA Accession No.: 1999-13566
Towards molecular farming in the future: using plant-cell-suspension cultures as bioreactors - for example **vector**-mediated tobacco transgenic plant construction, used for recombinant antibody, protein production, etc. **review**
AUTHOR: Fischer R; Emans N; Schuster F; Hellwig S; Drossard J
CORPORATE AFFILIATE: Tech.Coll.Aachen-Inst.Biol. Inst.Environ.Chem.Ecotox.Schmallenberg
CORPORATE SOURCE: Institut fuer Biologie, RWTH Aachen, Worringerweg 1, D-52074 Aachen, Germany.
JOURNAL: Biotechnol.Appl.Biochem. (30, Pt.2, 109-12) **1999**
ISSN: 0885-4513 CODEN: BABIET
LANGUAGE: English
ABSTRACT: Plant suspension cells are **reviewed** as an in vitro system for the production of recombinant protein under carefully controlled certified conditions. Free cell suspensions are considered to be the most suitable for large-scale applications in the biotechnology industry. Plant species used for generation and propagation of suspension cell cultures include Arabidopsis sp., Catharanthus sp., yew (Taxus sp.), **rice** (Oryza sativa), soybean (Glycine max), alfalfa (Medicago sativa) and tobacco (Nicotiana tabacum). Plant cell suspensions can be cultivated in shake flasks or culture vessel using batch, fed batch, perfusion and continuous culture. For recombinant protein production Agrobacterium sp. mediated **transformation**,

microparticle bombardment, electroporation of protoplasts or virus **vectors** can all be used. Tobacco suspension cell cultures have been used to express IgGs, Fab fragments, single chains, bispecific antibody fragments and fusion proteins. Tobacco BY-2 cells have been used for culture using a working volume of 40 l. A 10% (v/v) inoculum with a culture time of 150 hr produced a yield of 7.5 kg fresh cell weight. (52 ref)

WORD COUNT: 22407

ABSTRACT: Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in plants and play a major role in plant gene and genome evolution. In many cases, retrotransposons comprise over 50% of nuclear DNA content, a situation that can arise in just a few million years. Plant retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in plants compared to some other eukaryotes, including their often-high copy numbers, their extensively heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This **review** describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to plant genome evolution and their use as genetic tools in plant biology. Reprinted by permission of the publisher.

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04255630 H.W. WILSON RECORD NUMBER: BGSA00005630
Lentivirus replication and regulation.
AUGMENTED TITLE: **review**
Tang, Hengli
Kuhen, Kelli L; Wong-Staal, Flossie
Annual Review of Genetics v. 33 (1999) p. 133-70
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 17942

ABSTRACT: Lentiviruses are associated with chronic diseases of the hematological and neurological systems in animals and man. In particular, human immunodeficiency virus type 1 (HIV-1) is the etiological agent of the global AIDS epidemic. The genomes of lentiviruses are complex, encoding a number of regulatory and accessory proteins not found in other retroviruses. This complexity is reflected in their replication cycle, which reveals intricate regulatory pathways and unique mechanisms for viral persistence. In this **review,** we highlight some of these unique features for HIV-1, with particular focus on the transcriptional and posttranscriptional control of gene expression. Although our understanding of the biology of HIV-1 is far from complete, the knowledge gained thus far has already led to novel strategies for both virus intervention and exploiting the lentiviruses for therapeutic applications. Reprinted by permission of the publisher.

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04255140 H.W. WILSON RECORD NUMBER: BGSA00005140
Phylogenetic structure in the grass family (Poaceae): evidence from the nuclear gene phytochrome B.
Mathews, Sarah
Tsai, Rocky C; Kellogg, Elizabeth A
American Journal of Botany v. 87 no1 (Jan. 2000) p. 96-107
SPECIAL FEATURES: bibl il ISSN: 0002-9122
LANGUAGE: English